

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2003, 14:14:42 ; Search time 230 Seconds
(without alignments)

2084.096 Million cell updates/sec

Title: US-09-374-967-1

Perfect score: 1086

Sequence: 1 atgaagcccttcattc:tgt.....agcctgagatcgtcatgtga 1086

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapex: 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/FCRUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	399.6	36.8	1559	4	US-09-786-240-17
2	74.2	6.8	1535	3	US-09-032-372-8
3	73.2	6.7	787	4	US-09-007-119-20
4	58.4	5.4	7902	4	US-08-961-527-112
5	55.2	5.1	690	3	US-09-024-023-1
6	55.2	5.1	690	4	US-09-531-111-1
7	53.6	4.9	287	3	US-09-024-023-3
8	53.6	4.9	287	4	US-09-531-111-3
9	52.8	4.9	2634	1	US-08-196-218-31
10	52.8	4.9	2634	1	US-08-681-953-31
11	46.2	4.3	678	4	US-09-370-838-155
12	42.2	3.9	891	4	US-09-107-532A-2711
13	41.8	3.8	702	4	US-09-328-352-3686
14	41.6	3.8	6854	4	US-09-194-905-7
15	40.4	3.7	3571	4	US-09-221-017B-904
16	40.2	3.7	28804	2	US-08-592-874-1
17	40.2	3.7	28804	3	US-09-096-942-2
18	40.2	3.7	28804	3	US-09-096-867-2
19	39	3.6	960	4	US-09-252-991A-6944
20	39	3.6	1272	3	US-09-036-987A-28
21	39	3.6	1272	3	US-09-370-700-28
22	39	3.6	1272	4	US-09-603-207-28
23	39	3.6	1443	4	US-09-252-991A-6752
24	39	3.6	1695	4	US-09-252-991A-6801
25	38.2	3.5	164976	4	US-08-916-421B-1
26	37.4	3.4	5144	1	US-08-487-890A-105
27	37.4	3.4	5144	2	US-08-478-435-105

ALIGNMENTS

RESULT 1

US-09-786-240-17
; Sequence 17, Application US/09786240
; Patent No. 6558935
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592 PCT
; CURRENT APPLICATION NUMBER: US/09/786,240
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/150,657; unassigned; 09/186,779; unassigned; 60/133,642
; PRIOR FILING DATE: 1998-09-10; 1998-09-10; 1998-11-04; 1998-11-04; 1999-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 1559
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6558935 2682663CB1
US-09-786-240-17

Query Match 36.8%; Score 399.6; DB 4; Length 1559;
Best Local Similarity 61.1%; Pred. No. 6.8e-121;
Matches 664; Conservative 0; Mismatches 419; Indels 3; Gaps 1;

QY	1	ATGAAGCCCTTCATCTTGTTCGGGGTTTCGAAACCCGCTTCGGCCTTTGACTCTGAGC	60
DB	213	ATGAAGCCACTGATCTTAGTGGGGCTATGGAGCGGCTACGCGCGTGACGCTGAGC	272
QY	61	TTCCGGAACCCCTCGTGGATTTCGAAACAGCCCATGATTCTGCACCATCCAACT	120
DB	273	ACCCGAGCCACTGGTGGACTTCTTGCATATAGCCCTTCTGCTCCACCAAGTGGAGCG	332
QY	121	TTCAAAGAGTTGGGGTCACAGAGTGGTTTGGCTATCAACTATCGCCCAAGAGTAATG	180
DB	333	CTAGCGCGGCGAGCGTGACACCACTGATCTCGCGCGTGAGCTACATCTCGCAGGTGTG	392
QY	181	ATTATTTCTTGAAGGACTTTGAGGATTAAGTTGGCATCAACAATTACATGTCCCAAGAG	240
DB	393	GAGAAGGAATGAAGGCACAGGAGGCTGGGAATCCGAATCCGAATCTCCATGTCCCATGAA	452


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Db      533  TGCATCGTTGAGATCCACACACACAGGATTTGCACATATGTGGAGAACCCAGCACCA 592
Qy      499  TTTGTGGGTAAAGATCAATGCTGGGATTACTT 533
Db      593  TTTATCAGTCATCATCAATCAACTGGCGCATCTACCT 627

RESULT 3
US-09-007-119-20/c
; Sequence 20, Application US/09007119C
; Patent No. 6300541
; GENERAL INFORMATION:
; APPLICANT: Lightfoot, David A.
; APPLICANT: Gibson, Paul T.
; APPLICANT: Merkem, Khalid
; TITLE OF INVENTION: Soybean Sudden Death Syndrome Resistant Soybeans,
; TITLE OF INVENTION: Soybean Cyst Nematode Resistant Soybeans and Methods of
; TITLE OF INVENTION: Breeding and Identifying Resistant Plants
; FILE REFERENCE: Sou Illinois 1268/2 Sequence Listing
; Patent No. 6300541
; CURRENT APPLICATION NUMBER: US/09/007.119C
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035.335
; EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (152)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (162)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (173)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
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; LOCATION: (181)
; OTHER INFORMATION: (a or c or g or t/u)
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; NAME/KEY: misc_feature
; LOCATION: (228)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (265)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (292)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (329)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (335)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (339)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (363)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (384)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (387)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (396)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (400)..(401)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (421)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (428)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (432)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (462)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (475)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (514)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (521)
; OTHER INFORMATION: (a or c or g or t/u)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (526)
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	Query Match	6.7%	Score 73.2;	DB 4;	Length 787;
	Best Local Similarity	56.0%	Pred. No. 8.le-14;		
	Matches 227;	Conservative	0;	Mismatches 151;	Indels 27; Gaps 5;
QY	524	GGATTTACTTACTGAACCCCATCTGTCCTTCACCGCATTTGAGCTTGAGCCCAACATCATTC	583		
DL	563	GGGTAAACTCGATGAACCCCTTNGTATGGGAAGAAATNGAGNGACACACNNATTTCTTGGGA	504		

Query Match	5.4%	Score 58.4	DB 4	Length 7902
Best Local Similarity	52.5%	Pred. No. 2.3e-08		
Matches 128	Conservative 0	Mismatches 116	Indels 0	Gaps 0
Cy	2	TGAAGGCCTCATCTTGTGGGGGTTTCGAAACCGCCCTTCGGCCCTTGACTCTGAGCT	61	

Db 4961 TGAAGAGCATTATCTTAGCA3CGGGATTGGGAAGCTCGCTTGGCTCTATGACTGMAAATA 5020
Qy 62 TCCGGAACCCCTCGTGGATTTCGAACAAGCCCATGATTCTGCACAGATCGAGCTT 121
Db 5021 CCCCTAAAGCCTTGGTTTCAG3TTAATCAAAACCTTTGATTGAGTACCAAAATTGAGTTTC 5080
Qy 122 TGAAGAAGTTGGGGTCACAGAGTGGTTTGGGTATCAACTATCGCCCGAGAGTAAATGA 181
Db 5081 TCAAGAAGAAAGGAATCAAT3ACATCATCATGTTGGTTTATCTTAAAGAACAATTGC 5140
Qy 182 TTAATTTCTTGAAGGACTTTTGAAGTAAAGCTTGGCATCAACAATTACATGCTCCCAAGAGA 241
Db 5141 ATTACTTGAAGAGAAATAC3GTGTCGTCGTTTCAATGATAAATACGCTGACTACA 5200
Qy 242 CTGA 245
Db 5201 ATAA 5204

RESULT 5

US-09-024-023-1
; Sequence 1, Application US/09024023
; Patent No. 6110899
; GENERAL INFORMATION:
; APPLICANT: Lonetto, Michael A.
; TITLE OF INVENTION: licc
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,023
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/039,210
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-024-023-1

Query Match 5.1%; Score 55.2; DB 3; Length 690;
Best Local Similarity 51.6%; Pred. No. 6.1e-08;
Matches 126; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
Qy 2 TGAAGGCCCTCATTTCTTCGCGGGGTTTCGNAACCCGCTTCGGCCTTTGACTCTGAGCT 61
Db 2 TGAAGGCCATTATCTTAGCAGCGGGATTGGGAACCTCGCTTCGCTCTATGACTGAAATA 61
Qy 62 TCCGGAACCCCTCGTGGATTTCGAACAAGCCCATGATTCTGCACAGATCGAGCTT 121
Db 62 CCCCTAAAGCCTTGGTTTCAGGTTAATCAAAACCTTTGATTGAATACCAAAATTGAGTTTC 121

Qy 122 TGAAGAAGTTGGGTCACAGAGTGGTTTGGCTATCAACTATGCCCGAGGTAATGA 181
Db 122 TCAAGAAAAAGGAATCAATGACATCATCATCGTTGGTTATCTTTAAAGAACAAATTCG 181
Qy 182 TTAATTTCTTGAAGGACTTTGAGGATAAGCTTGGCATCACAATTTACATGCTCCCAAGAGA 241
Db 182 ATATTAAAGAAAAAATACGGTGTTCGCTCGTTTTCATGATAAATACGCTGACTACA 241
Qy 242 CTGA 245
Db 242 ATAA 245

RESULT 6

US-09-531-111-1
; Sequence 1, Application US/09531111
; Patent No. 6303571
; GENERAL INFORMATION:
; APPLICANT: Lonetto, Michael A.
; TITLE OF INVENTION: licc
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/531,111
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/024,023
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-531-111-1

Query Match 5.1%; Score 55.2; DB 4; Length 690;
Best Local Similarity 51.6%; Pred. No. 6.1e-08;
Matches 126; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
Qy 2 TGAAGGCCCTCATTTCTTCGCGGGGTTTCGGAACCCGCTTCGGCCTTTGACTCTGAGCT 61
Db 2 TGAAGGCCATTATCTTAGCAGCGGGATTGGGAACCTCGCTTCGCTCTATGACTGAAATA 61
Qy 62 TCCGGAACCCCTCGTGGATTTCGAACAAGCCCATGATTCTGCACAGATCGAGCTT 121
Db 62 CCCCTAAAGCCTTGGTTTCAGGTTAATCAAAACCTTTGATTGAATACCAAAATTGAGTTTC 121
Qy 122 TGAAGAAGTTGGGTCACAGAGTGGTTTGGCTATCAACTATGCCCGAGGTAATGA 181
Db 122 TCAAGAAAAAGGAATCAATGACATCATCATCGTTGGTTTATCTTTAAAGAACAAATTCG 181

QY 182 TTAATTTCTGAAGGACTTTGAGGATAAGCTTGGCATCAATACATGCTCCCAAGAGA 241
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Db 182 ATTATTTAAAGAAAATACGGTTCGCTCGTTTCAATGATAAATACGCTGACTACA 241
| | | | |
QY 242 CTGA 245
| | |
Db 242 ATAA 245

RESULT 7
US-09-024-023-3
; Sequence 3, Application US/09024023
; Patent No. 6110899
; GENERAL INFORMATION:
; APPLICANT: Lonetto, Michael A.
; TITLE OF INVENTION: licc
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,023
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/035,210
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-09-024-023-3
Query Match 4.9%; Score 53.6; DB 3; Length 287;
Best Local Similarity 51.2%; Pred. No. 1.2e-07;
Matches 125; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
QY 2 TGAAGGCCCTCATTTCTGTCGGGGGTTTCGGAACCCGCTTTCGGCCCTTGACTCTGAGCT 61
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Db 2 TGAAGGCCATTATCTTAGCAGCGGATTGGGAACCTCGCTTGCCTATGACTGAAATA 61
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QY 62 TCCCAAAACCCCTCGTGGATTTTGCAGAACCCCATGATTCGACACAGATCGAGCTT 121
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Db 62 CCCCTAAAGCCCTTGGTTTCAGGTTAATCAAAAACCTTTGATTGAATACCAAAATTCGATTTTC 121
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QY 122 TCAAGAGAGTTGGGTCACAGAGTGGTTTGGCTATCAACTATCGCCACAGATCGAGCTT 181
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Db 122 TCAAGAGAGAGGAAATCAATGACATCATCATCGTTGGTTTATCTTAAAGAACAAATTCG 181
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QY 182 TTAATTTCTGAAGGACTTTGAGGATAAGCTTGGCATCAATACATGCTCCCAAGAGA 241
| | | | |
Db 182 ATTATTTAAAGAAAATACGGTTCGCTCGTTTCAATGATAAATACGCTGACTACA 241
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QY 242 CTGA 245
| | |
Db 242 ATAA 245
| | |
RESULT 8
US-09-531-111-3
; Sequence 3, Application US/09531111
; Patent No. 6303571
; GENERAL INFORMATION:
; APPLICANT: Lonetto, Michael A.
; TITLE OF INVENTION: licc
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/531,111
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/024,023
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-531-111-3

Query Match 4.9%; Score 53.6; DB 4; Length 287;
Best Local Similarity 51.2%; Pred. No. 1.2e-07;
Matches 125; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
QY 2 TGAAGGCCCTCATTTCTGTCGGGGGTTTCGGAACCCGCTTTCGGCCCTTGACTCTGAGCT 61
| | | | |
Db 2 TGAAGGCCATTATCTTAGCAGCGGATTGGGAACCTCGCTTGCCTATGACTGAAATA 61
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QY 62 TCCCAAAACCCCTCGTGGATTTTGCAGAACCCCATGATTCGACACAGATCGAGCTT 121
| | | | |
Db 62 CCCCTAAAGCCCTTGGTTTCAGGTTAATCAAAAACCTTTGATTGAATACCAAAATTCGATTTTC 121
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QY 122 TGAAGAGAGTTGGGTCACAGAGTGGTTTGGCTATCAACTATCGCCACAGAGTAAATGA 181
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Db 122 TCAAGAGAGAGGAAATCAATGACATCATCATCGTTGGTTTATCTTAAAGAACAAATTCG 181
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QY 182 TTAATTTCTGAAGGACTTTGAGGATAAGCTTGGCATCAATACATGCTCCCAAGAGA 241
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Db 182 ATTATTTAAAGAAAATACGGTTCGCTCGTTTCAATGATAAATACGCTGACTACA 241
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QY 242 CTGA 245
| | |
Db 242 ATAA 245

RESULT 9
US-08-196-218-31
; Sequence 31, Application US/08196218
; Patent No. 5614619
; GENERAL INFORMATION:
; APPLICANT: Piepersberg, Wolfgang
; APPLICANT: Stockmann, Michael
; APPLICANT: Taleghani, Kampiz Mansouri
; APPLICANT: Distler, Jurgen
; APPLICANT: Grabley, Susanne
; APPLICANT: Sichel, Petra
; APPLICANT: Brau, Barbara
; TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
; TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and Their
; TITLE OF INVENTION: Use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,218
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: 36,223
; REFERENCE/DOCKET NUMBER: 03481.1372-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..401
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 416..1531
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1561..2625
US-08-196-218-31

Query Match 4.9%; Score 52.8; DB 1; Length 2634;
Best Local Similarity 57.1%; Pred. No. 8.4e-07;
Matches 96; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 1 ATGAAGGCCCTCATCTTGTGGGGTTTCGAAACCCGCTTCGGCCTTTGACTCTGAGC 60
Db 1561 ATGAAGGCTCTGGTCTGCGCGGGATCTCGTACCCGCTTCGGCCTTTGACTCTGAGC 1620
Qy 61 TTCCCGAAACCCCTCGTGGATTTTGCAACAAAGCCCATGATCTGCACACAGATCGAAGCT 120
Db 1621 ATGCCAAACAACTGATCCCATGCCAACACACCCGCTGCTGGTCATGCTGCTGAAGCC 1680
Qy 121 TTGAAGAAGTTGGGTCACAGAGTGTTTGGCTATCAACTATCGC 168

Db 1681 GTCCGGAGCTGGCGTGCACCGAGGTGCGCGTCATCGTCGCAACCGC 1728

RESULT 10
US-08-681-953-31
; Sequence 31, Application US/08681953
; Patent No. 5710032
; GENERAL INFORMATION:
; APPLICANT: Piepersberg, Wolfgang
; APPLICANT: Stockmann, Michael
; APPLICANT: Taleghani, Kampiz Mansouri
; APPLICANT: Distler, Jurgen
; APPLICANT: Grabley, Susanne
; APPLICANT: Sichel, Petra
; APPLICANT: Brau, Barbara
; TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
; TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and Their
; TITLE OF INVENTION: Use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,953
; FILING DATE: 30-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/196,218
; FILING DATE: 25-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: 36,228
; REFERENCE/DOCKET NUMBER: 02481.1372-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..401
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 416..1531
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1561..2625
US-08-681-953-31

Query Match 4.9%; Score 52.8; DB 1; Length 2634;
Best Local Similarity 57.1%; Pred. No. 8.4e-07;
Matches 96; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 1 ATGAAGGCCCTCATCTTGTGGGGTTTCGAAACCCGCTTCGGCCTTTGACTCTGAGC 60
Db 1561 ATGAAGGCTCTGGTCTGCGCGGGATCTCGTACCCGCTTCGGCCTTTGACTCTGAGC 1620
Qy 61 TTCCCGAAACCCCTCGTGGATTTTGCAACAAAGCCCATGATCTGCACACAGATCGAAGCT 120

Db 1621 ATGCCCAACAACTGATCCCATGCCAACACACCCGGTGGTGTGCTGAACGCC 1683
QY 121 TTGAAGAAGTGGGGTACAGAGTGTGTTTGGTATCACTATCGC 168
Db 1691 GTCCGGAGTGGGGTGTGACGAGGTGGCGTGCATGCTGGCAACGCC 1728

RESULT 11

US-09-370-838-155
; Sequence 155, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; EARLIER FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version: 3.0
; SEQ ID NO 155
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-155

Query Match 4.3%; Score 46.2; DB 4; Length 678;

Best Local Similarity 49.5%; Pred. No. 5.5e-05;
Matches 151; Conservative 0; Mismatches 148; Indels 6; Gaps 1;

- QY 235 CAAGAGACTGAGCCCTTAGGAAACCCCTGCTCTAGCAAGGCAAGCTGCG 294
Db 350 CAGGAATTTGCCCCCTAGGCACAGGGGTGCTTTACCATTTTCGAGACCATCTG 409
QY 295 GATGATCTGGCCAGCCATTCTTTGCTCTCAACAGTGTATGAAGCGAATACCCATT 354
Db 410 GCTGGAGCCCGAGGCACTTCTTCGTCTCAATGCTGATGCTGCTCGACTTCCCTTG 469
QY 355 GCTGAACATCATCAATTTCPAAGTGTATGTTGTGTGAGGCAACATATGCTACTAAG 414
Db 470 AGTGCTATGTTGGAAGCCCPCCGAGCCGAGCTACCCCTTTCTACTCCTTGGCACTACG 529
QY 415 GTGGATG-----AACCATCAAAATACGCTGTTGTGTTATGGAGGCAACTGGCAGG 468
Db 530 GCTAACAGGACCATCCCTCAACTACGGCTGCATCGTTGAGATCCACAGACACAG 589
QY 469 GTGGAAGGTTTGTGAGAGCCAAATAATTGTTGGGTAAACAAGATCAATGCTGGGATT 528
Db 590 GTATTGCATATGTGGAGAAACCAGCACATTTATCAGTGACATCATCAACTGGGCACC 649
QY 529 TACTT 533
Db 650 TACCT 654

RESULT 12

US-09-107-532A-2711
; Sequence 2711, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street

CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2711:
SEQUENCE CHARACTERISTICS:
LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (8) LOCATION 1...891
SEQUENCE DESCRIPTION: SEQ ID NO: 2711:
US-09-107-532A-2711

Query Match 3.9%; Score 42.2; DB 4; Length 891;

Best Local Similarity 55.9%; Pred. No. 0.0013;
Matches 80; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGAAGGCCCTCATCTCTCGGGGTTTCGAAACCCGCTTCGGCCTTTGACTCTGAGC 60
Db 25 ATGAAGGGAATCATCTCTCGGGGCGAGCGCAACACGCTCTGTACCCCTTAAACAAAGCA 84
QY 61 TTCCCGAAACCCCTCGTGGATTTTCAACACAGCCCATGATCTGCACAGATCGAAGCT 120
Db 85 ACATCGAAACAATTGATGCCGATTTATGACAAACCAATGATTTATTCCAATGCTACT 144
QY 121 TTGAAGAAGTGGGGTCAACAGA 143
Db 145 CTGATGTTGGCGGAATCAAGA 167

RESULT 13

US-09-328-352-3686
; Sequence 3686, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 9252
; SEQ ID NO 3686
; LENGTH: 702
; TYPE: DNA

; ORGANISM: Acinetobacter baumannii
US-09-328-352-3686

Query Match 3.8%; Score 41.8; DB 4; Length 702;
Best Local Similarity 50.8%; Pred. No. 0.0016;
Matches 100; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1 ATGAGGCCCTCATCTTGTGCGGGGTTTCGGAACCGCCTTCGGCGCTTTGACTCTGAGC 60
DB 13 ATGAAGCAATGATTTTAGCTGTGCTGGCTTGGCAATCGTATGGTCCACTACACTATAT 72
CY 61 TTCCCGAAGCCCTCGTGGGATTTTGCAACAAGCCCATGATTTGCAACCAAGT-CGAAGCT 120
DB 73 ACACCAAGCCTCTGCTTGAAGTAGGGGTAAAGCACTATTGTGGCATATTGAAAA 132
QY 121 TTGAAGAAGTTGGGTCACAGAGTGGTTTGGCTATCAACTATACGCCAGAGGTAATG 180
DB 133 CTTAAGAAAATCGGTGACGAAATAGTCATCAATTCGTGGTGTAGCAGACAACTC 192
QY 181 ATTAATTTCTGAAGGA 197
DB 193 ATCAGTAGCTGGGAGA 209

RESULT 14

US-09-194-905-7
; Sequence 7, Application US/09194905
; Patent No. 6306827
; GENERAL INFORMATION:
; APPLICANT: DECKER, Heinrich
; TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR
; TITLE OF INVENTION: PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS
; TITLE OF INVENTION: GLA.O AND THEIR USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/M3-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/194,905
; FILING DATE: 29-JUL-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/02826
; FILING DATE: 30-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19622783.6
; FILING DATE: 07-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 026083/0193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-194-905-7

Query Match 3.8%; Score 41.6; DB 4; Length 6854;

Best Local Similarity 55.6%; Pred. No. 0.0071;
Matches 80; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 2 TGAAGGCCCTCATCTTGTGCGGGGTTTCGGAACCGCCTTCGGCGCTTTGACTCTGAGCT 61
DB 2269 TGAAGGCCCTCGTCTGCGAGGTGGAACCGGAGCAGACTGAGGCGGTTTCAACCCACACCG 2328
QY 62 TCCGAAACCCCTCGTGGATTTTGCAAAACAGCCCATGATTTGCAACAGATCGAAGCTT 121
DB 2329 CGCCCAAGCAGCTGCTCCCACTCGCCCAACAGCCCGTCTCTTCTACGCGTGGAGTCCC 2388
QY 122 TGAAGAAGTTCGGGTCACAGAGG 145
DB 2389 TCGCCGCGCGGGTGTCCGGAGG 24:2

RESULT 15

US-09-221-017B-904
; Sequence 904, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: ROSS, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 904:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: 1...3571
US-09-221-017B-904

Query Match      3.7%; Score 40.4; DB 4; Length 3571;
Best Local Similarity 43.3%; Pred.No. 0.012;
Matches 240; Conservative 0; Mismatches 311; Indels 3; Gaps 1;

QY 1 ATGAAGGCCCTCATCTTCGCGGGGTTTCGGAACCCGCGCTTCGGCCTTTGACTCTGASC 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 89 ATGAAGGAATAATCTTCGCGAGGATCCGGCACCTCGTCTATATCCGATAACTCGGGGT 148

QY 61 TTCCCCGAACCCCTCGTGTGATTTTGCACAACAGCCGATGATCTGCACACAGATCGAAGCT 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 149 GTGAGCAAAACAGCTTCTACCCGTTTATGACAAAGCCGATGATTTACTACCCGCTTCTACG 208

QY 121 TTCAAGAGAGTTGGGGTCAAGAGGTGGTTTTGGGTATCAACTATCGCCAGAGGTAATG 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 209 CTTATGCTTGGGGTATTTCGGGATGTCCTGATCAITTCACGCCGAGGACTTATCCATG 268

QY 181 ATTAAATTTCTGAAGACTTTGAGGATAAGCTTTGGGATCACAATTAATGCTCCCAAGAG 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 269 TTCCAACGGCTATTGGGTGATGGCGGTGATCTCGGTGTCGGTTCGGGTGAGGTATGCAAGCAA 328

QY 241 ACTGAGCCCTTAGGAACCGCTGCGCCTCTTGCTTAGCAAGGGACAAGCTTGGGATGGA 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 329 CCTCCCGGATGGATGGCACAGGCTTTTCATCTCGGACGTGAATTTGTAGGAGCGAT 388

QY 301 TCTGGCCAGCCATTCTTTGCTCAACAGTGTATGTCATAAGCGAATACCCATTTGCTGAA 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 389 TGTGCTGTCTCGTCTTAGAGATAATAATCTTCTAGGGCATGGCTTCAGCCAAATGCTT 448

QY 361 CTCATCAAAATTTCAAGATGTCATGGTGTGAGGCAACAATTTATGTCACCTAAGGTGAT 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 449 CGGTGCGCAGTTGCCGATCGGAAAAGGGTATGGCCACCAITTTTCGGCTATTATGTGAAT 508

QY 421 GAACCATCAAAATACCGTGTGTGGTTATGGAGGAGGCAACTGGCAGGGTGGAAAAGTTT 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 509 GATCCTGAGCGATACGGTGTAGCGG---AAGTGGATGCTACCGGCAAGGTCAATCAGCCTG 565

QY 481 GTTGAGAACCAAAATATTTTGGGTAAACAAGATCAATGCTGGGATTTACTACTGAAC 540
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 566 GAAGAAAAACCGGAAAAAGCGGAAGAGCAACTACGCAGTAGTGGGACTCTATTTCATGCC 625

QY 541 CCATCTGTCTTGA 554
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Db 626 AATGTGTACTTGA 639
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Job time : 237 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 10:53:48 ; Search time 362 Seconds

(without alignments)
7784.434 Million cell updates/sec

Title: US-09-374-967-1

Perfect score: 1086

Sequence: 1 atgaagccctcattcttgt.....agctgagatcgctgta 1086

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690.8	63.6	1109	12	US-10-342-224-23
2	399.6	36.8	1559	12	US-10-427-631-17
3	360.8	33.2	1095	14	US-10-128-714-7009
4	310.8	28.6	1089	12	US-10-032-585-6223
5	247.6	22.8	1051	14	US-10-128-714-1009
6	247.6	22.8	1370	14	US-10-128-714-6009
7	247.6	22.8	3051	14	US-10-128-714-9
8	247.6	22.8	3370	14	US-10-128-714-5009
9	241.6	22.2	960	14	US-10-128-714-2009
10	187	17.2	218	9	US-09-294-093B-2164
11	180.8	16.6	488	11	US-09-770-961-719
12	151.4	13.9	364	10	US-09-878-574-2725
13	130.6	12.0	269	10	US-09-878-574-8673
14	79.2	7.3	272	10	US-09-878-574-10462
15	74.6	6.9	2493	14	US-10-156-761-6955
16	74.6	6.9	9025608	14	US-10-156-761-1

c	17	73.2	6.7	787	10	US-09-954-773A-20	Sequence 20, Appl
	18	64.2	5.9	456	10	US-09-796-692-5169	Sequence 5169, Ap
	19	64.2	5.9	456	14	US-10-040-862-5169	Sequence 5169, Ap
	20	55.2	5.1	282	9	US-09-294-093B-3871	Sequence 3871, Ap
	21	50.8	4.7	1080	14	US-10-156-761-5021	Sequence 5021, Ap
	22	46.2	4.3	678	10	US-09-738-973-155	Sequence 155, App
	23	46.2	4.3	678	10	US-09-854-133-155	Sequence 155, App
	24	46.2	4.3	678	14	US-10-144-649A-155	Sequence 155, App
	25	42.8	3.9	6158	12	US-10-292-198-1	Sequence 1, Appli
	26	41.6	3.8	6854	10	US-09-922-683-7	Sequence 7, Appli
	27	41.2	3.8	386	11	US-09-918-995-7323	Sequence 7323, Ap
	28	39	3.6	474	11	US-09-918-995-24581	Sequence 24581, A
	29	38	3.5	167343	9	US-09-962-436-281	Sequence 281, App
	30	38	3.5	167343	10	US-09-964-824A-273	Sequence 273, App
	31	37.8	3.5	897	14	US-10-156-761-935	Sequence 935, App
	32	37.8	3.5	9025608	14	US-10-156-761-1	Sequence 1, Appli
	33	37.6	3.5	2840	12	US-10-114-153-3	Sequence 3, Appli
	34	37.4	3.4	2115	14	US-10-128-714-7238	Sequence 7238, Ap
	35	37.4	3.4	5144	14	US-10-043-344-105	Sequence 105, App
	36	36.8	3.4	536165	11	US-09-939-964-1	Sequence 1, Appli
	37	36.6	3.4	1179	14	US-10-156-761-7119	Sequence 7119, Ap
	38	36.4	3.4	855	10	US-09-738-626-371	Sequence 371, App
	39	36.4	3.4	3309400	10	US-09-738-626-1	Sequence 1, Appli
	40	36	3.3	317	14	US-10-146-938-10	Sequence 10, Appli
	41	35.8	3.3	4699	14	US-10-043-344-1	Sequence 1, Appli
	42	35.6	3.3	1830121	14	US-10-329-960-1	Sequence 173, App
	43	35.4	3.3	3119	11	US-09-975-719-173	Sequence 19, Appli
c	44	35.2	3.2	808	10	US-09-954-773A-19	Sequence 11, Appli
	45	35.2	3.2	879	10	US-09-861-289-11	

ALIGNMENTS

RESULT 1

US-10-342-224-23
; Sequence 23, Application US/10342224
; Publication No. US20030162294A1
; GENERAL INFORMATION:
; APPLICANT: Nathalie Verbruggen
; TITLE OF INVENTION: Genes Involved in Tolerance to Environmental Stress
; FILE REFERENCE: CN-012US
; CURRENT APPLICATION NUMBER: US/10/342,224
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US/09/762,154
; PRIOR FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: EP 98202634.6
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1109
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)....(1107)
US-10-342-224-23

Query Match 63.6%; Score 690.8; DB 12; Length 1109;
Best Local Similarity 77.3%; Pred. No. 6.7e-220;
Matches 839; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

QY	1	ATGAGGCCCTCATTCTTGTTCGGGGGTTTCGAAACCGCCTTCGGCCTTGACTCTGAGC	60
DB	22	ATGAGGGCACTCATCTTTGTTCGGACCTTCGGACCTTCGACCATTCGACTCTCAGT	81
QY	61	TTCCCGAAACCCCTCGTGGATTTCGAAACAGCCATGATTCGACCATCGAAGCT	120
DB	82	TTCCCGAAACCCCTCGTGGATTTCGAAACAGCCATGATTCGACCATCGAAGCT	141
QY	121	TTGAAAGAGTGGGGTTCACAGAGTGGTTTGGCTATCAACTCGCCAGAGGTAATG	180

Db 142 CTTAAGCAGCTTGAGTTGATGAAGTGGTTTGGCCATCAATTATCAGCCAGAGGTGATG 201
Qy 181 ATTAATTTCTGAAGGACTTTAGGATAAGCTTTGGCATCAAAATTACATCTCCCAAGAG 240
Db 202 CTGAACCTTTCTGAAGGACTTTAGACCAAGCTGGAAATCAAAATCACTTGTCTCACAAGAG 261
Qy 241 ACTGAGCCCTTAGGAACCGCTGGCCCTCTTCTCTAGCAAGGACAGCTTGGCGATGA 300
Db 262 ACCGAGCCACTAGTAGCCGCTGGCTCTAGCGAGAGCAAAATTTGCTTGATGA 321
Qy 301 TCTGGCAGCCATTTCTTTGTCTCAACAGTGTATCTATAAGCGAATACCCATTTGCTGAA 360
Db 322 TCTGGAGGCCCTTTCTTTGTCTTAAAGTGTATAGTAGTACCTCTTTAAAGAA 381
Qy 361 CTATCAAAATTTCAAGTGTCATGGTGGTGAAGCAAAATTTAGTCACTAAAGGTGAT 420
Db 382 ATGCTTGAGTTTCAAAATCTCAGCGTGGGAGAGCCCTCCATATATGGTAAACAAAGGTGAT 441
Qy 421 GAACCATCAAAATACGGTGTGTGTTTATGGAGGAGCAACTGCGAGGTGGAAAGTTT 480
Db 442 GAACCGTCGAAATATGAGTGTGTTTATGGAGAAAGCACTGGAAGAGTGGAGAAATTT 501
Qy 481 GTTGAGAGCCAAATAATTTGTGGGTAAACAGATCAATGCTGGGATTTACTTACTGAAC 540
Db 502 GTGGAAGCCAAATCTATGTAGGTAAACAGATCAACGCTGGGATTTATCTTCTGAAC 561
Qy 541 CCATCTGCTTGAACCGATTTAGCTGAGGCAACATCAATTTGAGAAAGAGGTCTTCCCT 600
Db 562 CCATCTGCTTGAATAAGATTAGCTAAGACCGACTTCAATCGAAAGAGAGACTTTCCT 621
Qy 601 CAATTCAGCTGATCAACAACCTATGCAATGCTCTCCAGTCTTCCAGTCTTTGAGTGGATTT 660
Db 622 AAGATTTTCAGGAGCGCAAGGCTCTATGCTATGGTGTACCAAGGTTTGGATGGACATTT 681
Qy 661 GGTGAGCTAGGACTACATTTACTGCTGCTGCTTTATCTAGACTCGATTTAGAGAGAA 720
Db 682 GGGCAACCCCGTGACTACATNAACGGGTTTGAGACTCTTACTTACTTCCCTTAGAGAGAA 741
Qy 721 TCAGTCCCAAGCTAGCTACTGAGACACATGTTGTTGGCAATGCTGTTGCTGATGAGAGC 780
Db 742 TCTCTGCCAAATTAACCAAGTGGGCCACACATAGTTGGGAATGTTCTTGTGACGAACC 801
Qy 781 GCCAAGATTGAGAGGTTGTCTGATTTGCTCATGCTGCCATTTGGACCTGGGTGTT 840
Db 802 GCTACAAATGGGAGAGATGTTGATTTGACACAGCTTGCCATTTGTCTCCAGGCTGCATTT 861
Qy 841 GTGAGGACGGCTGAGGCTTTCCCGCTGCACTGTCAATGCGCGCGTGCCTATCAAGAG 900
Db 862 GTTGAGTCAGGAGTCAGACTCTCCCGATGCAGGTCATGCTGGAGTCCGCATCAAGAG 921
Qy 901 CATGCTTGATCTCAACAGCAATTTATCGGCTGGCACTCAACTGTTGTGATGAGAGAG 960
Db 922 CATCGGTGATCTCGAGCAGTATCATCGGCTGGCACTCAACGGTGTGATGAGAGAG 981
Qy 961 ATAGAGATATGATATCTCTCGGAGAGATGTTTCATGTTGTGATGAGGTGTACAGCAAT 1020
Db 982 ATCGAGAACATGAGATCTCTCGTGAAGATGTTTCATGTTGAGCGATGAGATCTATAGCAAT 1041
Qy 1021 GCGGCTGTTGTTTCCACACAATAAGAGATCAAGTCAAGCAATTTGAGAGCTGAGATCGTC 1080
Db 1042 GGAGGAGTTGTTTGGCCACACAAGAGATCAAAATCAAAACATCTTTGAGAGCCAGAGATG 1101
Qy 1081 ATGTGA 1086
Db 1102 ATGTGA 1107

RESULT 2

US-10-427-631-17

; Sequence 17, Application US/10427631

; Publication No. US20030175923A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;

; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
; APPLICANT: BAUGHN, Mariah R.; LAL, Preeti G.;
; APPLICANT: YUE, Henry; HILLMAN, Jennifer L.;
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSPERASE PROTEINS
; FILE REFERENCE: PF-0592-1 DIV
; CURRENT APPLICATION NUMBER: US/10/427,631
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 09/786,240
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US99/20989
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 60/172,220
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/155,248
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/133,642
; PRIOR FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERU Program
; SEQ ID NO 17
; LENGTH: 1559
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030175923A1 2682663CB1
US-10-427-631-17

Query Match 36.8%; Score 399.6; DB 12; Length 1559;
Best Local Similarity 61.1%; Pred. No. 2.2e-122; Indels 3; Gaps 1;
Matches 664; Conservative 0; Mismatches 419;
Qy 1 ATGAAGGCCCTCAATCTTGTGCGGGGTTTGGAAACCCGCTTTCGGCCTTTGACTCTGAGC 60
Db 213 ATGAAGGCACTGATCTTAGTGGGGGCTATGGAGCGGCTACGCGCGTACGCTGAGC 272
Qy 61 TTCCCGAAACCCCTCGTGGATTTTCAACAACAGCCCATGATCTCGACCAAGATCAAGCT 120
Db 273 ACCCCGAAGCCACTGCTGGACTCTGCAATAAGCCCATCTTGTGCAACCAAGTGGAGCG 332
Qy 121 TTGAAGAAGTTGGGTCACAGAGTGGTTTGGCTATCAACTATCGCCACAGGTTAATG 180
Db 333 CTAGCGCGGAGGCGTGGACCCAGTGATCTTGGCCGTGAGCTACATGTCGAGAGTGTG 392
Qy 181 ATTAATTTCTGAAGGACTTTTGAAGATAAGCTTGGCATCAAAATTACATGCTCCCAAGAG 240
Db 393 GAGAAGGAAATGAAGGCACAGGACAGAGGCTGGGAATCCGAATCTCCATGTCCCATGAA 452
Qy 241 ACTGAGCCCTTAGGAACCGCTGGCCCTTGTCTCTAGCAAGGACAAAGTTCGCGATGA 300
Db 453 GAGGAGCCCTTGGGACACACTGGGCCCTTGGCGCTGGGCCCGTGAACCTACTCTC---TGAG 509
Qy 301 TCTGGCCAGCCATTTCTTGTCTCAACAGTGTATGTCATAAGCGAATACCCATTTGCTGAA 360
Db 510 ACTGACAGCCCTTTCTTGTCTCTCAACAGTACGTCATCTGCGATTTCCCTTCCAAACC 569
Qy 361 CTCATCAAAATTTCAAGTGTCTATGGTGGAGCAAAATTTATGTCATTAAGTGTGAT 420
Db 570 ATGGTGACGTTCCACCGGCACCATGCCAGGAGGCTCCATCCTGTCACCAAGGTGAG 629
Qy 421 GAACCATCAAAATAGCGTGTGTTGTTATGAGGAGGCAACTGGCAGCGGTGGAAAGTTT 480
Db 630 GAACCCCTCCAAGTACGGTGTGTTGTTGAGGCTGACACAGGCCCGCATTCACCGTTTC 689
Qy 481 GTTGAGAGCCAAATAATTTGTGGTTAACAGATCAATGCTGGGATTTTACTTACTGAAC 540
Db 690 GTGGAGAGCCACAGGTGTTGTGTCCCAATAGATCAACGAGGCGATGTACATCTTGAGC 749
Qy 541 CCATCTGCTTTGACCGCATTTGAGCTGAGGCGCAACATCAATTTGAGAAAGAGGTCTTCCCT 600
Db 750 CTGCGAGTGTCTCGCGCGCATCCAGCTGGCAGCTACGTCCA-TGAGAAGAGAGTCTTCCCC 809

QY 1069 CTTGAGATCGTCATGTGA 1086
 ||||| |||||
 Db 1078 CTTGCCATTATCATGTGA 1095

RESULT 4

US-10-032-585-6223
 ; Sequence 6223, Application US/10032585
 ; Publication No. US20030180953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Terry, Roemer D.
 ; APPLICANT: Bo, Jiang
 ; APPLICANT: Charles, Boone
 ; APPLICANT: Howard, Bussey
 ; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
 ; FILE REFERENCE: 10182-005-999
 ; CURRENT APPLICATION NUMBER: US/10/032,585
 ; NUMBER OF SEQ ID NOS: 8000
 ; CURRENT FILING DATE: 2001-12-20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6223
 ; LENGTH: 1089
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 ; US-10-032-585-6223

Query Match 28.6%; Score 310.8; DB 12; Length 1089;
 Best Local Similarity 57.2%; Pred. No. 9.2e-93;
 Matches 624; Conservative C; Mismatches 457; Indels 9; Gaps 3;

QY 1 ATGAAGCCCTCATCTTGTGGGGTTTGGACCGGCTTCGGCTTTGACTCTGAGC 60
 ||||| |||||
 Db 1 ATGAAGAGGATTAATTAGTTCGGAGGATACGGTACCAGATTGAGACCAATTAACTTAAAC 60
 61 TTCCGGAACCCCTCGTGAATTTTGAACAACGCCCATGATTCTGCACAGATCGAAGCT 120
 61 TTACCAAAACCATTTGGTCGATTCGGTACAGACCAATGATCTTGACCAATCGAAGCT 120
 QY 121 TTGAAGAAGTTGGGTACAGAGTGGTTTGGCTATCAACTATCGCCAGAGGTAATG 180
 - Db 121 TTGGCCGCTGCTGCTCACCGATATTTGTTTGGCGTCAACTACCGTCCAGAACTATG 180
 181 ATTAATTTCTTGAAGACTTTGAGGATAGCTTGGCATCACAAATACATCTCCCAAGAG 240
 181 GTTCCACTTTAAGAAATACGAAGAAGATACGGTGTCTCCATCACCTCTCTGTTGAA 240
 QY 241 ACTGAGCCCTTAGGAACCGCTGCGCTCTTGTCTTAGCAAGGAGCAAGCTTCGGATGGA 300
 Db 241 GAAGAACCCTTTGGGCACCGCGGTCCATTAAAGTTGGCTGAAGAAGTGT---GAAAAA 297
 QY 301 TCTGGCCAGCCATCTTTGTCCTACAGTGTGTCATGAAGCAATACCCATTCTCTGAA 360
 Db 298 GAGACTTCACATTTTCGTCCTTGAACCTCGAGCTATTTGGAGCTACCCATTCAAGGAA 357
 QY 361 CTCATCAAAATTTCAAGTGTCTATGTTGGTGAAGCAACAATATGTCACCTAAGTGGAT 420
 Db 358 TTGGCCGACTTCACAAAGGCCACCGCGTGTGCTGTTGTTGCTACCAAGTCCAC 417
 QY 421 GAACCATCAAAATACGGTGTGTTGGTTATGGA---GGAGGCACTGGCAGGGTGAAGG 477
 Db 418 GAACCATCAAAATACGGGTCATTGTCCACGACAGACACTCCAAACTTGTATCGACAGA 477
 QY 478 TTGTTGAGAAGCCAAAAATATTGTTGGGTAAACAAGATCAATGCTGGGATTTTACTTCTG 537
 Db 478 TTGTTGAAAAAACGAGTCGAGTTTGTGTAACAGAAATTAACGCCGTTTATACATCTTG 537
 QY 538 AACCATCTCTCTTGAACCGCATTTGAGCTGAGGCCAACATCAATTTGAGAAAGAGTCTTC 597
 Db 538 AACCATCTGCTCATCGACTTGTATTGAATGAGACCAACCTCAATCGAAAAAGAACTTTC 597
 QY 598 CCTCAAAATTCGAGCTGATCAACAGCTCTATGCAATGGTCTCTCCAGGTTTGGATGAT 657
 ||||| |||||

Db 598 CCAATCTTGGTGGAAACAAAAACAATTGTACTCTCTCGACTTGGAGGGTTACTGGATGAC 657
 QY 658 GTTGTTCAGCCTAGGAGCTACATTACTTGGCTTGGCTCTTTTACTAGACTCGATTAGGAAG 717
 ||||| |||||
 Db 658 GTGGGTCACACCAAAAGATTTCCTTTCTGAAACCTGTTTGTACTTGAAGTCTTTCGAAA 717
 QY 718 AAATCAGCTGCCAAGCTAGCTACTGAGCACATGT---TGTGGCAATGTCTGCTGTCAT 774
 ||||| |||||
 Db 718 AAACACCCAGAGAAATTTGTGTAAAGAGAAATACGTCCATGGCGGTAACTGTTGATCGAC 777
 QY 775 GAGAGCGCCAAAGATTGGAGAGAGTTGTCTGATTGGTCTCTGATTCGCAATTGGACCTGGG 834
 ||||| |||||
 Db 778 CCAACTGCCCAAGATCAACCCATCTCTCTTAATCGGTCCAAACGTCACCATCGGTCCAAAC 837
 QY 835 TGTGTTGTGGAGACGGGTGAGGCTTTCCCGCTGCACGTCTATCGCGCGGCTGCGTATC 894
 838 GTTGTGTCTGGTGAAGGTGCTAGAAATCCAAAGATCAGTGTGTTGGCCCACTCCCAAGTC 897
 QY 895 AAGAGCATGCTTGATCTCAACAGCATTTATCGGCTGGGCTCAACTGTGTTGGTCAATGG 954
 ||||| |||||
 Db 898 AAAGACCCAGCGCTGGGTCAAAATCTACCATTTGTTGGTTGGAACCTCCAGAAATTGGAAGTGG 957
 QY 955 GCACGGATAGAAATATGACTATCTCGGGGAGGATGTTCAATGTTGTGTGATGAGGTGAC 1014
 ||||| |||||
 Db 958 GCTAGAACTGAAGGTGTTTACCGTCTTGGGTGACGACGTGGAAGTGAAGAAACGAAATCTAC 1017
 QY 1015 AGCAATPGCGGTGTTGTTCTCCACATAAAGAGATCAAGTCAAGCATTTCTGAAGCTGAG 1074
 1018 GTCAACGGTGCCAAGGTCTTGGCCACACAAATCGATCTCTCTTCAAGCTGGAAGAAAGTCT 1077
 QY 1075 ATCGTCACTGT 1084
 ||||| |||||
 Db 1078 ATCAATTATGT 1087

RESULT 5

US-10-128-714-1009
 ; Sequence 1009, Application US/10128714
 ; Publication No. US2003011903A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Hu, Weng
 ; APPLICANT: Tishkoff, Daniel
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Eroshkin, Alexey M
 ; APPLICANT: Lemieux, Sebastien Y
 ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
 ; FILE REFERENCE: 10182-018-999
 ; * CURRENT APPLICATION NUMBER: US/10/128,714
 ; CURRENT FILING DATE: 2002-04-23
 ; PRIOR APPLICATION NUMBER: US 60/285,697
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: US 60/287,066
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/295,890
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/303,899
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/316,362
 ; PRIOR FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 86C3
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1009
 ; LENGTH: 1051
 ; TYPE: DNA
 ; ORGANISM: Aspergillus fumigatus
 ; US-10-128-714-1009

Query Match 22.8%; Score 247.6; DB 14; Length 1051;
 Best Local Similarity 57.9%; Pred. No. 1.3e-71;
 Matches 521; Conservative 0; Mismatches 364; Indels 15; Gaps 4;

174	QY	174	GGTAAATGATTAAATTTCTTGAAGGACTTTGAGGATAAGCTTGGCAATCAACAATTACATGCTC	233
70	DB	70	GCTAAATCTGCAATTTGTGCCCGCAGTAGTACGAGGAAACAATAACAAGCTCAGAATTCGATGTTCTC	129
234	QY	234	CCAAGAGACTGAGCCCTTAGSAAACCGCTGGCCCTCTTGCTCTACGAAGGACAAGCTTGC	293
130	DB	130	CGTGGAGTCCGAACCCCTCGGTACCGCTGGTCCCTGAAGCTGGCA--GAGAAGATTTT	186
294	QY	294	GGATGGATCTGGCCAGCCATCTTTTGTCTCAACAGTGAATGTCTAATAGCGAATACCCATT	353
187	DB	187	GGGCAAGAGACGATTTCTCCCTCTTTCGTTCTCAACTCCGATATCATCTGTGATATCCCTT	246
354	QY	354	TGCTGTAACATCAAAATTCACAAGTCTCATGTGGTGGAGGACACAATATATGTCACATA	413
247	DB	247	TAAACAGCTCGCAGAGTTCCAAGAAGAACATGGCGACGAGGGCACCATCTGTTGTTACCAA	306
414	QY	414	GGTGGATGAACCATCAAAATACGGTGTGTGGT---TATGGAGGAGGCAACTGGCAGGGT	470
307	DB	307	GGTCGACGAGCCCTCGAAGTACGGTGTGTTGTCCAACAAGCCCAACCATCCCTCTCGCAT	366
471	QY	471	GGAAGAGTTTGTGAGAAGCCAAAATAATTTGTGGGTAAACAAGATCAATGCTGGGATTTA	530
367	DB	367	TGATCTGTTTCGTCCGAGAAGCCAGTTGAGTTGCTTGGTAACCGCATTAACGCCGGATCTCA	426
531	QY	531	CTTACTCAACCCCATCTGCTCTTGACCGCATTGAGCTGAGGCCAACATCAATTTGAGAAAGA	590
427	DB	427	CATCCTCAACCCCTAGTGTCTCAAGCGCATTTGAGCTGGTCTTACTCCATCGAACAGGA	486
591	QY	591	GGTCTTCCCTCAAAATTCGAGCTGATCAACAGCTCTATGCAATGTGCTCTCCAGGTTTTTG	650
487	DB	487	GACATTTCCCGCCCATCTGCAACGGACGGTCACTCCACTCTTTGATCTCGAGGGTTTTCTG	546
651	QY	651	GATGGATGTTGGTCAGCCCTAAGGACTACATTACTGGCTTGCGTCTTTTATCTAGACTCGAT	710
547	DB	547	GATGGATGTTGGTCAACCCCAAGATTTCTGACGGGCACTGCGCTCTACCTCGGCTCGCT	606
711	QY	711	TAGGAAGA-----AATCAGCTGCCAAGCTAGCTACTGGAGCACATGT-TGTTGGCAA	761
607	DB	607	CGCGAAGCGGTAACTCCAAGCTGTGTGGCCCCCAACAGCGAGCGGTACGTCTACGCGGCAA	666
762	QY	762	TGTGCTGCTGCATGAGAGCGCAAGATTGGAGAAGTTGTTGATGGTCTCTGATGTCGC	821
667	DB	667	CGTCATGGTTGATCCCTCGGCAAGATCGGCAAGAACTGTCCGATTTGGCCCTATCTAGT	726
822	QY	822	CATTGGACCTGGGTGTGTTGGAGGACGGCGTGAAGGCTTCCCGCTGCACTGTCAATCGC	881
727	DB	727	CATTGGTCCCAACGTTGTGGTGGCGATGGCGTGGCTCTGCAACGCTGTGTGCTCTTGA	786
882	QY	882	CGGCGTCCGTTCAAGAAGCATGCTTGCATCTCAACACAGCATTTATCGGTGGGCACTCAAC	941
787	DB	787	GAACAGCAAGGTCGAAGACCAATGCTTGGATCAAGTCGACTATTGTCGGTTGGAACAGCTC	846
942	QY	942	TGTTGGTCAATTGGCACGGATAGAGAATATGACTATCTCGGGGAGGATGTTTCATGTGTG	1001
847	DB	847	CGTTGGCAAGTGGGCTCGCTTGGAGAATGTACCGGTCTTGGGTGACGATGTACCATTTGC	906
1002	QY	1002	TGATGAGGTGTACAGCAATGCGGTGTGTTCTCCCATAAAGAGATCAAGTCAAGCAT	1061
907	DB	907	TGACGAGGTGTATGTAATGACGGCTCTATTCTCCGCAACGAAGAGCATCAAGCAAGACAT	966

RESULT 6

```

US-10-128-714-6009
; Sequence 6009, Application US/10128714
; Publication NO. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

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Query Match	22.8%;	Score 247.6;	DB 14;	Length 3370;
Best Local Similarity	57.9%;	Pred. No. 2.6e-71;		
Matches 521;	Conservative	0;	Mismatches 364;	Indels 15; Gaps 4;
QY	174	GGTAANTGATTAATTTCTTGAAGGACITTTGAGGATAGCTTTGGCATCAATTCATGCTC	233	
Db	1389	GCTAAATCTGCAATTTGTGCCCGCAGTAGTACGAGGAACAATACAACGTCAGAAATCGAGTTCTC	1448	
QY	234	CCAAGAGACTGAGCCCTTAGTAAACCGCTGGCCCTCTTGTCTTAGTACGAGGACAAAGCTTGC	293	
Db	1449	CGTCGAGTCCGAACCCCTCGTAGCCGCTGGTCCCTGAAGTGGCA---GAGAAAGATTTC	1505	
QY	294	GGATGGATCTGGCGAGCCATCTTTTGTCTCAACAGTGTATGTATAGCGAAATACCCATT	353	
Db	1506	GGCAAGAGGACGATTCCTCCCTTCCTCGTTCTCAATCCGATATCATCTGTATTATCCCTT	1565	
QY	354	TGCTGAACCTCATCAAAATTTACAGTGTCTATGTTGGTGGAGCAACAATATATGTCCTAA	413	
Db	1566	TAAAGAGCTCGCAGAGTTCCACAAGAAACATGCGCAGCGGGGACCCATCGTTGTTACCAA	1625	
QY	414	GGTGGATGAACCATCAAAATACGGTGTGTGGT---TATGGAGAGGCAACTGGCAGGT	470	
Db	1626	GGTCGACGAGCCCTCGAAGTAGGTTGCTGTGTGCCACAAGCCCAACCATCCCTCTCGCAT	1685	
QY	471	GGAAAGTTTGTGTGAGAGGCCAAAATATTTTGGGTAAACAAGATCAATGCTCGGATTTA	530	
Db	1686	TGATCGTTTTCGTCCGAAAGCTAGTTGAGTTTCGTTGGTTAACCGGANTAAACGCCGATCTA	1745	
QY	531	CTTACTGMACCCATCTGTCTTCACCGCATGTAGCTGAGGCCACATCAATTTGAGAAAGA	590	
Db	1746	CATCCTCAACCCCTAGTGTTCACAAGCGCATGTAGCTGCGTCTTACCTCCATCGAACAGGA	1805	
QY	591	GGTCTTCCCTCAAATTTGCAGTTGATCAACAGCTCTATGCAATGCTCTCCAGGT-TTTG	650	
Db	1806	GACATTTCCCGCCCATCTGCATCGAGCTCAGCTCCATCTCTTTGATCTCGAGGGTTCTG	1865	
QY	651	GATGGATGTTGGTCAGCCTAAGGACTACATTAATGGCTTCGCTTTTATCTAGACTCGAT	710	
Db	1866	GATGGATGTTGGTCAACCCAAAGATTTCCTGAAGGACCTGCTCTACCTCGCTCGCT	1925	
QY	711	TAGGAGA-----AATCAGCTGCCAAGCTAGCTACTGGAGCACATGT-TGTTGGCAA	761	
Db	1926	CGGAAGCGTAACTCCAAAGCTGTGGCGCCCAACAGCGAGCCGTAGCTACCGCGGCAA	1985	
QY	762	TGTGCTGGTGCATGAGAGCGTCAAGATTGGAGAAGGTTGTCTGATTGGTCTCATGTGCG	821	
Db	1986	CGTCATGTTGATCCCTCGTCAAGATCGCAGAACCTGTGCGATTGGCCCTTAATGTAGT	2045	
QY	822	CATTGACCTGGGTGTGTTGTGGAGGACGGGTGAGGCTTTCCCGCTGCACTGTCTATGCG	881	
Db	2046	CATTGTTCCCAACGTTGTGTGTCGGCGATGCGGTGCGTCTGCAACGCTGTGTCTTTGGA	2105	
QY	882	CGGCGTGCGTATCAAGAAGCATGCTTGCATCTCAACAGCATTTATCGGCTGGCACTCAAC	941	
Db	2106	GAAACGAAGGTCAAGGACCACTGCTTGGATCAAGTCGACTATTTGTTCGTTTGGAACTGTC	2165	
QY	942	TGTTGGTCAAATGGGCACGGATAGAGAATATGACTATCTCGGGGAGGATGTTTCATGTGTG	1001	
Db	2166	CGTTGCAAGTGGGCTCGCTGGAGATGTCAAGGCTCTTGGGTGACGATCTCACCATTGC	2225	
QY	1002	TGATGAGGTGTACAGCAATGTCGGTGTGTTTCTCCCAATATAAGAGATCAAGTCAAGCAT	1061	
Db	2226	TGACGAGGTGTATGTCAATGTCGGCTCTATTTCTGCCCCACAAGAGCATCAAGCAGAACAT	2285	

RESULT 9

US-10-128-714-2009

; Sequence 2009, Application US/10128714

; Publication No. US20030119013A1

; GENERAL INFORMATION:

APPLICANT: Jiang, Bo

; APPLICANT: Hu, Wenqi

```

1  APPLICANT: Tishkoff, Daniel
2  APPLICANT: Zarudio, Carlos
3  APPLICANT: Eroshkin, Alexey M
4  APPLICANT: Lemieux, Sebastien M
5  TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
6  TITLE OF INVENTION: Methods of Use
7  FILE REFERENCE: 10182-018-999
8  CURRENT APPLICATION NUMBER: US/10/128,714
9  CURRENT FILING DATE: 2002-04-23
10 PRIOR APPLICATION NUMBER: US 60/285,697
11 PRIOR FILING DATE: 2001-04-23
12 PRIOR APPLICATION NUMBER: US 60/287,066
13 PRIOR FILING DATE: 2001-04-27
14 PRIOR APPLICATION NUMBER: US 60/295,890
15 PRIOR FILING DATE: 2001-06-05
16 PRIOR APPLICATION NUMBER: US 60/303,899
17 PRIOR FILING DATE: 2001-07-09
18 PRIOR APPLICATION NUMBER: US 60/316,362
19 PRIOR FILING DATE: 2001-08-31
20 NUMBER OF SEQ ID NOS: 8603
21 SOFTWARE: PatentIn version 3.1
22 SEQ ID NO 2009
23 LENGTH: 960
24 TYPE: DNA
25 ORGANISM: Aspergillus fumigatus
26 US-10-128-714-2009

```

Query Match 22.2%; Score 241.6; DB 14; Length 960;
Best Local Similarity 58.5%; Pred. No. 1.2e-69;
Matches 500; Conservative 0; Mismatches 339; Indels 15; Caps 4;

Qy	220	ACAA	TACATGCTCC	CAGAGACTGAGCCCTTAGGAA	CCGCTGGCCCTCTTGCTCTAGCA	279
Db	25	AGAAT	CGAGTCTCCGTCGAGTCCGAA	CCGCTCGGTACCGCTCGTCCCTTGAAGACTGGCA	84	
Qy	280	AGGACAAGCTTCGGATCGAT	CTGGCCAGCCATCTTTGTCTCTCAACAGTGTATGCATA	339		
Db	85	--	-GAGAGATT	TGGCAGGACGATTCTCCCTCTTCGTCTCAACTCCGATATCATC	141	
Qy	340	AGGGAATACCCA	TTTGCTGAACTCATCAAA	TTTCACAAGTGTGATGGTGTGAGGCAACA	399	
Db	142	TGTGATTATCCCTTTAAGCAGCTCGCAGAGTCTCCA	CAAGAAACATGCGCAGCAGGGGACC	201		
Qy	400	ATTATGGTCACTAAGGTGGATGAACCATCAAAATACGGTCTTGCTGGT	--TATGGAGGAG	456		
Db	202	ATCGTGTATACAAAGGTCGACGAGCCCTCGAAGTACGGTGTCTGT	CTCCACAAGCCCAAC	261		
Qy	457	GCAACTGGCAGGCTGGAAAGGTTGTGTGAGAGCCCAAAAATATTTGTGGGTACACAGATC	516			
Db	262	CATCCCTCTCCGATGTATCTCTTCGTGTGAGAGCCAGTTGAGTTCGTGTGTACCCGCAAT	321			
Qy	517	AATGCTGGGATTTACTTACTTGAAACCCATCTGTCTCTGACCGCATTTGAGCTGAGGCGCAACA	576			
Db	322	AACGCGGTATCTACATCTCAACCCCTAGTGTCTCAAGCGCATTGAGCTGCGTCTTACC	381			
Qy	577	TCAAATTGAGAAAGAGGCTTCCCTCAAAATGACGTGATCAACAGCTCTATGCAATGGTC	636			
Db	382	TCCATCGAACAGGAGACATTTCCCGCCCATCTGACGGCAGCGTCAGCTCCACTCCTTTGAT	441			
Qy	637	CTTCCAGGTTTTTGGATGGATGTTGGTTCAGCCTTAGGGACTACATACTGGCTTGGCGTCTT	696			
Db	442	CTCGAGGTTTCTGGATGGATGTTGGTCAACCCAAAGATTTCTCTGACGGGCACTCGCTC	501			
Qy	697	TATCTAGACTCGAATTAGGAAGA-----AA	TCACTGCCAAGCTAGTACTTGGAGCAC	748		
Db	502	TACCTCGCCTCGCTCGAAGCGTAATCTCAAGCTCTGCGCCCAACACGACGACGCTAC	561			
Qy	749	ATGT-TGTTGGCAATGTCTGGTGTGCATGAGAGCGGCCAAGATTCGGAAGGTTCTCTGATT	807			
Db	562	GTCTACGGCGCAAGCTCATGGTTGATCCCTCGGCCAAGATCGGCAAGAACTGTTCGCAAT	621			
Qy	808	GGTCCTGATCTGCCCATTTGGACCTGGGTGTGTTGTGGAGGACGGCTGAGGCTTTCCCCG	867			

Db 622 GCCCCTAATGTAGTCATTGGTCCCAACGTTGTGGTGGCGATGGCGTGGCTCTGCAACGC 681
Qy 868 TGCACCTGTTCATCGCGGGTGGTATCAAGAAAGCATGCTTCGATCTCAAAACAGCACTATC 927
Db 682 TGTGTGCTCTTGGAGAACAGCAAGGTCAAGACCATGCTTGGATCAAGTCGACTATTGTC 741
Qy 928 GCGTGGCACTCAACTGTGGTCAATGGCGACGGATAGAGAAATAGCTATCTCTGGGGAG 987
Db 742 GGTGGAAACAGCTCCGTTGGCAAGTGGGCTCGCTTGGAGAAATGTCAAGGTCTGGGTGAC 801
Qy 988 GATGTTCAATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1047
Db 802 GATGTCACATGCTGTGACGAGGTGATGTCATGCGCGCTCTATTCTGCCGCCCAAGAGC 861
Qy 1048 ATCAAGTCAAGCAT 1061
Db 862 ATCAAGCAGACAT 875

RESULT 10

US-09-294-093B-2164
; Sequence 2164, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 2164
; LENGTH: 212
; TYPE: DNA
; ORGANISM: Zea mays
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700345651H1
; NAME/KEY: unsure
; LOCATION: 129
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-2164

Query Match 17.2%; Score 187; DB 9; Length 212;
Best Local Similarity 98.6%; Pred. No. 8,6e-52;
Matches 209; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Qy 558 CATTGAGCTGAGCCCAACATCAATTTGAGAAAGAGTCTTCCTTCAAATTGCACTGATC 616
Db 2 CATTGAGCTGAGCCCAACATCAATTTGAGAAAGAGTCTTCCTTCAAATTGCACTGATC 61
Qy 617 AACAGCTCTATGCAATGCTCTTCAGGTTTTCAGTGTGTTGATGATGTTGTCAGCTAGGACT 676
Db 62 AACAGCTCTATGCAATGCTCTTCAGGTTTTCAGTGTGTTGATGATGTTGTCAGCTAGGACT 121
Qy 677 ACATTACTGGCTTGGCTCTTTATCTAGACTCGATTAGGAAGAAATCAGCTGCCAAGCTAG 736
Db 122 ACATTACNGGC-TGGCTCTTTATCTAGACTCGATTAGGAAGAAATCAGCTGCCAAGCTAG 180
Qy 737 CTACTGGAGCACATGTTGTTGCAATGTGCTG 768
Db 181 CTACTGGAGCACATGTTGTTGCAATGTGCTG 212

RESULT 11

US-09-770-961-719/c
; Sequence 719, Application US/09770961
; Publication No. US20030115639A1
; GENERAL INFORMATION:

; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Broeze J.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2026 (PARA-015PRV)
; CURRENT APPLICATION NUMBER: US/09/770,961
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,466
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 719
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-961-719

Query Match 16.6%; Score 180.8; DB 11; Length 488;
Best Local Similarity 80.3%; Pred. No. 1.7e-49;
Matches 212; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 823 ATTGACCTGGGTGTGTGTGGAGACGGGTGAGGCTTTCGGCTGCACGTGTCATGGC 882
Db 488 ATTGTCCAGGCTGCATTGTTGAGTCAGAGTCAGACCTCCCGATGACGGTCATGGT 429
Qy 883 GCGTGGCTATCAAGAAGTCCTGCATCTCAACAGCATTCGGCTGGCACTCAACT 942
Db 428 GGAGTCCGCATCAAGAAGTCGGTGTATCTCGAGCAGTATCATCGGTGGCAGCTCAACG 369
Qy 943 GTTGTCAATGGGCACGATAGAGAAATATGACTATCCTGGGGAGGATGTTTCATGTGT 1002
Db 368 GTTGTCAATGGGCACGATCGAGAAATGAGGATCCTCGGTGAGGATGTTTCATGTGAGC 309
Qy 1003 GATGAGGTGACAGCAATGGGGTGTGTTCTCCACATAAAGAGATCAAGTCAAGCAAT 1062
Db 308 GATGAGTCTATAGCAATGGAGGAGTGTGTTTGGCCACAGAGAGATCAAAATCAAAATC 249
Qy 1063 CTGAAGCTTGAGATCGTCATGTGA 1086
Db 248 TTGAAGCCAGAGATAGTATGTGA 225

RESULT 12

US-09-878-574-2725
; Sequence 2725, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535

; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 2725
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-021-Q1-B1-C7
US-09-878-574-2725

Query Match 13.9%; Score 151.4; DB 10; Length 364;
Best Local Similarity 74.3%; Pred. No. 9.8e-40;
Matches 191; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
Qy 1 ATGAAGCCCTCATCTCTGTGGGGGTTTCGGAACCCGCTTCGGCTTTGACTCTGAGC 60
Db ATGAAGCCCTCATCTCTGTGGGGGTTTCGGAACCCGCTTCGGCTTTGACTCTGAGC 60
Qy 108 ATGAAGCCCTCATCTCTGTGGGGGTTTCGGAACCCGCTTCGGCTTTGACTCTGAGC 167
Db ATGAAGCCCTCATCTCTGTGGGGGTTTCGGAACCCGCTTCGGCTTTGACTCTGAGC 167
Qy 61 TTCCCGAAACCCCTCGTGGATTTCGAAACAGCCCATGATTCGACACGATCGAAGCT 120
Db TTCCCGAAACCCCTCGTGGATTTCGAAACAGCCCATGATTCGACACGATCGAAGCT 120
Qy 121 TTGAAGAAGTTGGGTCACAGAGTGTGTTTGGCTATCAACTATCGCCGAGAGTAATG 180
Db TTGAAGAAGTTGGGTCACAGAGTGTGTTTGGCTATCAACTATCGCCGAGAGTAATG 180
Qy 228 CTTAAGGCCATTGGAGTCACTAGGTAGTGTGCTAGCCATCAATTACCAACCAAGAGTATG 287
Db CTTAAGGCCATTGGAGTCACTAGGTAGTGTGCTAGCCATCAATTACCAACCAAGAGTATG 287
Qy 181 ATTAATTTCTTGAAGGCTTTGAGGATAAGCTTGGCATCAATTCATCTCCCAAGAG 240
Db ATTAATTTCTTGAAGGCTTTGAGGATAAGCTTGGCATCAATTCATCTCCCAAGAG 240
Qy 288 TTGAATTTCTTGAAGGATTGTAATCAAGCTCGGCATCAAGATCACATGTTCTCAGGAA 347
Db TTGAATTTCTTGAAGGATTGTAATCAAGCTCGGCATCAAGATCACATGTTCTCAGGAA 347
Qy 241 ACTGAGCCCTTAGGAAC 257
Db ACTGAGCCCTTAGGAAC 257
Qy 348 ACTGAACCACTGGGAAC 364
Db ACTGAACCACTGGGAAC 364

RESULT 13
US-09-878-574-8673
; Sequence 8673, Application US/09378574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 8673
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701101510H1
US-09-878-574-8673

Query Match 12.0%; Score 130.6; DB 10; Length 269;
Best Local Similarity 70.3%; Pred. No. 7.4e-33;
Matches 189; Conservative 0; Mismatches 79; Indels 1; Gaps 1;
Qy 230 GCTCCCAAGAGACTGAGCCCTTAGGAACCGCTGGCCCTCTTGCTCTAGCAAGGCAAGC 289
Db GCTCCCAAGAGACTGAGCCCTTAGGAACCGCTGGCCCTCTTGCTCTAGCAAGGCAAGC 289
Qy 290 TTGGGATGGATCTGGCC-AGCCATCTTTTCTCTCAACAGTATGTCATGAAGCAATAC 348
Db TTGGGATGGATCTGGCC-AGCCATCTTTTCTCTCAACAGTATGTCATGAAGCAATAC 348
Qy 61 TGATAGTCACTCTGGAGAACCTTTTGTCTCAACAGTATGTTATCAGTGAGTAT 120
Db TGATAGTCACTCTGGAGAACCTTTTGTCTCAACAGTATGTTATCAGTGAGTAT 120
Qy 349 CCATTGCTGAACCTCATCAATTTTCAACAGTGTCTGCTGAGGCAACAATTTATGTC 408
Db CCATTGCTGAACCTCATCAATTTTCAACAGTGTCTGCTGAGGCAACAATTTATGTC 408
Qy 121 CCATCAAGAAGATGATTGAATTCATCAAAACCATGAGGAGGCTTCATTAATGGTA 180
Db CCATCAAGAAGATGATTGAATTCATCAAAACCATGAGGAGGCTTCATTAATGGTA 180

Qy 409 ACTAAGTGGATGAACCATCAAAATACGGTCTTGTGTTATGGAGGAGCAACTGGCAGG 468
Db ACTAAGTGGATGAACCATCAAAATACGGTCTTGTGTTATGGAGGAGCAACTGGCAGG 468
Qy 181 ACCAAGTGTGACGAGCCATCAAAAGTACGGCTGTTGTATGGAAGAGACACAGGCGAG 240
Db ACCAAGTGTGACGAGCCATCAAAAGTACGGCTGTTGTATGGAAGAGACACAGGCGAG 240
Qy 469 GTGGAAGGTTTGTGGAAGCCCAAAAT 497
Db GTGGAAGGTTTGTGGAAGCCCAAAAT 497

RESULT 14
US-09-878-574-10462
; Sequence 10462, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 10462
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700966702H1
US-09-878-574-10462

Query Match 7.3%; Score 79.2; DB 10; Length 272;
Best Local Similarity 72.9%; Pred. No. 1.2e-15;
Matches 102; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
Qy 1 ATGAAGCCCTCATCTCTGTGGGGGTTTCGGAACCCGCTTCGGCTTTGACTCTGAGC 60
Db ATGAAGCCCTCATCTCTGTGGGGGTTTCGGAACCCGCTTCGGCTTTGACTCTGAGC 60
Qy 132 ATGAAGCCCTCATCTCTGTGGGGGTTTCGGAACCCGCTTCGGCTTTGACTCTGAGC 191
Db ATGAAGCCCTCATCTCTGTGGGGGTTTCGGAACCCGCTTCGGCTTTGACTCTGAGC 191
Qy 61 TTCCCGAAACCCCTCGTGGATTTCGAAACAGCCCATGATTCGACACGATCGAAGCT 120
Db TTCCCGAAACCCCTCGTGGATTTCGAAACAGCCCATGATTCGACACGATCGAAGCT 120
Qy 192 TTCTCAAGCCCTCTGTTGATTTCGTAACAAACCTAGATTCTGCATCAGATAGAGGCC 251
Db TTCTCAAGCCCTCTGTTGATTTCGTAACAAACCTAGATTCTGCATCAGATAGAGGCC 251
Qy 121 TTGAAGAAGTTGGGCTCAC 240
Db TTGAAGAAGTTGGGCTCAC 240

RESULT 15
US-10-156-761-6955
; Sequence 6955, Application US/10:56761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10:156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6955
; LENGTH: 2493
; TYPE: DNA

; ORGANISM: Streptomyces avermectilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2493)
US-10-156-761-6955

Query Match 6.9%; Score 74.6; DB 14; Length 2493;
Best Local Similarity 51.5%; Pred. No. 1.6e-13;
Matches 254; Conservative 0; Mismatches 224; Indels 15; Gaps 3;

Qy	1	ATGAAGGCCCTCATTTGTGGGGTTTCGGAAACCGCCCTTCGGCCCTTTGACTCTGAGC	60
Db	1	ATGAAGGCCGTCGTGATGGCCGGAGCGAAGGCACACGCCCTTCGCCGATGACTCGAGT	60
Qy	61	TTCCCGAAACCCCTCGTGGATTTCGAAACAAAGCCCATGATTCGACACAGATCGAAGCT	120
Db	61	ATGCCCAAGCGCTCTCTGCCCTGTTAAACCGGCCGATCATGGAGCATGTCTCGGCTTA	120
Qy	121	TTGAAAGAAGTTGGGGTCACAGAGGTGTTTGGCTATCAACTATCGCCAGAGGTAATG	180
Db	121	CTCAAAAGGATGGGCTCAAGAGACGTCGTAACCTGTGCAGTTCCTGGCGTCTCTCGTC	180
Qy	181	ATTAATTTCTTGAAGGACTTTGAGGATAAGCTTGGCATCAATTAATGCTCCCAAGAG	240
Db	181	AAGAACTACTTCGGTGAC---GGCGAAGAGCTCGCATGGAGCTCACTTATGCCAATGAG	237
Qy	241	ACTGAGCCCTTAGAAGCGCTGGCCCTCTTGCTCTAGCAAGGACACAGCTTGGGATGGA	300
Db	238	GAGAAGCCACTCGGTACCGCTGGGAGCGTCAAGAACCGCGAGGAAGCGCTGAAGGA---	293
Qy	301	TCTGGCCAGCCATTCTTTGTCTCAACAGTGTATCATAGCGAATACCCATTGTGTAA	360
Db	294	-----CGACACTTTCCTCGTCACTCCGGTGATGCCCTGACCGACTTCGATCTCACCGAG	348
Qy	361	CTCATCAAAATTCAAAGTGTCATGGTGGTGAGGCAACAATTTGGTCACTAAGGTGGAT	420
- Db	349	CTGATCAATTTCCACAAGGAAGGGTGCGCTGCTCACCGTCTGTCTGACGCGGTGCC	408
Qy	421	GAACCATCAAAATACGGTGTGTGGTTATGGAGGAGGCAACTGSCAGGGTGGAAAGTTT	480
Db	409	AATCCTCTGGAATTCGGCATACCATCGTCGACGAGAA---GGCAAGGTCGAGCGCTTC	465
Qy	481	GTTGAGAAGCCAA	493
Db	466	CTCGAGAAGCCCA	478

Search completed: October 15, 2003, 11:00:17
Job time : 376 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:03:06 ; Search time 31 Seconds
(without alignments)
1876.366 Million cell updates/sec

Title: US-09-374-967-2

Perfect score: 1864
Sequence: 1 MKALLIVGGFGRRLRPLTLUS.....GVVLPKHKIKSLKPEIVM 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1681	90.2	361	12	US-10-342-224-24 Sequence 24, Appl
2	1681	90.2	361	12	US-10-427-631-32 Sequence 32, Appl
3	1183.5	63.5	360	12	US-10-427-631-2 Sequence 2, Appl
4	1161.5	62.3	364	15	US-10-128-714-8009 Sequence 8009, Ap
5	1099.5	59.0	362	12	US-10-032-585-7223 Sequence 7223, Ap
6	1045	56.1	373	12	US-10-427-631-33 Sequence 33, Appl
7	878.5	47.1	319	15	US-10-128-714-3009 Sequence 3009, Ap
8	515	27.6	831	15	US-10-156-761-14505 Sequence 14505, A
9	488	26.2	359	10	US-09-712-363-269 Sequence 269, App
10	469.5	25.2	360	15	US-10-156-761-12571 Sequence 12571, A
11	431.5	23.1	348	10	US-09-738-626-4325 Sequence 4325, Ap
12	314	16.8	355	12	US-09-769-734-33 Sequence 33, Appl
13	296	15.9	355	10	US-09-922-683-10 Sequence 10, Appl
14	281.5	15.1	237	15	US-10-156-761-8552 Sequence 8552, Ap
15	277.5	14.9	453	10	US-09-925-637-18 Sequence 18, Appl

16	277.5	14.9	453	15	US-10-084-205-18	Sequence 18, Appl
17	275.5	14.8	449	9	US-09-815-242-5479	Sequence 5479, Ap
18	275.5	14.8	452	9	US-09-815-242-12149	Sequence 12149, A
19	257.5	13.8	243	15	US-10-156-761-11498	Sequence 11498, A
20	247.5	13.3	237	15	US-10-156-761-7906	Sequence 7906, Ap
21	239	12.8	146	10	US-09-738-973-190	Sequence 190, App
22	239	12.8	146	10	US-09-854-133-190	Sequence 190, App
23	239	12.8	146	15	US-10-144-649A-190	Sequence 190, App
24	228.5	12.3	224	11	US-09-975-719-175	Sequence 175, App
25	227	12.2	456	9	US-09-815-242-10400	Sequence 10400, A
26	216.5	11.6	458	9	US-09-815-242-11759	Sequence 11759, A
27	216	11.6	456	9	US-09-815-242-14064	Sequence 14064, A
28	209	11.2	456	9	US-09-815-242-11073	Sequence 11073, A
29	198.5	10.6	299	15	US-10-156-761-8485	Sequence 8485, Ap
30	195.5	10.5	748	12	US-10-032-585-7314	Sequence 7314, Ap
31	194.5	10.4	285	10	US-09-738-626-3871	Sequence 3871, Ap
32	190	10.2	292	10	US-09-861-289-12	Sequence 12, Appl
33	190	10.2	292	10	US-09-860-846-12	Sequence 12, Appl
34	190	10.2	292	11	US-09-988-184B-12	Sequence 12, Appl
35	190	10.2	292	11	US-09-836-821-12	Sequence 12, Appl
36	190	10.2	292	11	US-09-793-708-14	Sequence 14, Appl
37	190	10.2	292	12	US-10-201-365-16	Sequence 16, Appl
38	190	10.2	292	12	US-10-160-535-14	Sequence 14, Appl
39	190	10.2	3782	10	US-09-861-289-4	Sequence 4, Appl
40	190	10.2	3782	10	US-09-860-846-4	Sequence 4, Appl
41	190	10.2	3782	11	US-09-988-384B-4	Sequence 4, Appl
42	190	10.2	3782	11	US-09-836-821-4	Sequence 4, Appl
43	189.5	10.2	461	9	US-09-815-242-10937	Sequence 10937, A
44	188	10.1	485	10	US-09-738-626-4551	Sequence 4551, Ap
45	187.5	10.1	456	12	US-10-326-185-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-10-342-224-24
; Sequence 24, Application US/10342224
; Publication No. US20030162294N1
; GENERAL INFORMATION:
; APPLICANT: Nathalie Verbruggen
; TITLE OF INVENTION: Genes Involved in Tolerance to Environmental Stress
; FILE REFERENCE: CNN-012US
; CURRENT APPLICATION NUMBER: US/10/342,224
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US/09/762,154
; PRIOR FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: EP 98202634.6
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-342-224-24

Query Match	90.2%	Score 1681	DB 12	Length 361
Best Local Similarity	98.6%	Pred. No. 6e-169		
Matches 320	Conservative 22	Mismatches 19	Indels 0	Gaps 0
QY	1	MKALLIVGGFGRRLRPLTLSPFKPLVDFAFKPMILHQIEALKEVGVTEVVLAINRPEVM	60	
DB	1	MKALLIVGGFGRRLRPLTLSPFKPLVDFAFKPMILHQIEALKEVGVTEVVLAINRPEVM	60	
QY	61	INFLKDFEDKLGITITSCQETEPGLTAGPLALARDKLADSGQPFVLSNDVISEYFAE	120	
DB	61	LNFLKDFETKLEIKITSCQETEPGLTAGPLALARDKLADSGQPFVLSNDVISEYPLKE	120	
QY	121	LKPKHCHGGGATINVTKVDEPSKYGVVWMEATGRVERVEKPKIFVGKINAGIYLLN	180	
DB	121	MLEPKHSGGGEASINVTKVDEPSKYGVVWMEESTGRVEKPKLYVGKINAGIYLLN	180	

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QY 181 PSVLDRLELPTSTIEKEVFPQIAADQOLYAMVLPGFMMVGGQPRDYITGLRLYLDLSIRKK 240
Db 181 PSVLDRLELPTSTIEKETFPKIAAAQOLYAMVLPGFMMVGGQPRDYITGLRLYLDLSIRKK 240
QY 241 SAAKLATGAHVGNVNLVHESAKIGEGCLIGPDVAIGPGCVVDEGVRLSRCTVMRGVRIKK 300
Db 241 SPAKLTSGPHVGNVNLVDETTATIGEGCLIGPDVAIGPGCVVDEGVRLSRCTVMRGVRIKK 300
QY 301 HACISNSIIGHSTVGOWARIEENMTILGEDVHVCDEVYNSGGVVLPHKKEIKSSILKPEIV 360
Db 301 HACISSIIIGHSTVGOWARIEENMTILGEDVHVCDEVYNSGGVVLPHKKEIKSNILKPEIV 360
QY 361 M 361
Db 361 M 361

RESULT 2
US-10-427-631-32
; Sequence 32, Application US/10427631
; Publication No. US20030175923A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
; APPLICANT: BAUGHN, Mariah R.; LAL, Preeti G.;
; APPLICANT: YUE, Henry; HILLMAN, Jennifer L.;
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592-1 DIV
; CURRENT APPLICATION NUMBER: US/10/427,631
; CURRENT FILING DATE: 2003-04-23
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US99/20989
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: US 60/172,220
; PRIOR FILING DATE: 1998-09-10
; PRIOR FILING DATE: 1998-11-04
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20030175923A1 g2642159
US-10-427-631-32

Query Match 90.2%; Score 1681; DB 12; Length 361;
Best Local Similarity 88.68; Pred. No. 6e-169;
Matches 320; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKALILVGGFGRRLRPLTSLSPKPLVDFANKPMILHQIEALKEGVGVTEVVLAINYRPEVM 60
Db 1 MKALILVGGFGRRLRPLTSLSPKPLVDFANKPMILHQIEALKEGVGVTEVVLAINYQPEVM 60
QY 61 INFLKDFEDKLGITITCSQTEPLEGTAGLALARDKLADGSGQPPFFVLNSDVISSEYPPAE 120
Db 61 INFLKDFETKLEIKITCSQTEPLEGTAGLALARDKLADGSGQPPFFVLNSDVISSEYPLKE 120
QY 121 LIKFKHCHGGEATIMVTKVDSPSKYGVVWMEATGRVERFVEKPKIFVGNKINAGIYLLN 180
Db 121 MLEFKHSHGGEASIMVTKVDSPSKYGVVWMEESGRVEKPKIFVGNKINAGIYLLN 180
QY 181 PSVLDRLELPTSTIEKEVFPQIAADQOLYAMVLPGFMMVGGQPRDYITGLRLYLDLSIRKK 240
Db 181 PSVLDRLELPTSTIEKETFPKIAAAQOLYAMVLPGFMMVGGQPRDYITGLRLYLDLSIRKK 240
QY 241 SAAKLATGAHVGNVNLVHESAKIGEGCLIGPDVAIGPGCVVDEGVRLSRCTVMRGVRIKK 300
Db 241 SPAKLTSGPHVGNVNLVDETTATIGEGCLIGPDVAIGPGCVVDEGVRLSRCTVMRGVRIKK 300
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Db 241 SPAKLTSGPHVGNVNLVDETTATIGEGCLIGPDVAIGPGCVVDEGVRLSRCTVMRGVRIKK 300
QY 301 HACISNSIIGHSTVGOWARIEENMTILGEDVHVCDEVYNSGGVVLPHKKEIKSSILKPEIV 360
Db 301 HACISSIIIGHSTVGOWARIEENMTILGEDVHVCDEVYNSGGVVLPHKKEIKSNILKPEIV 360
QY 361 M 361
Db 361 M 361

RESULT 3
US-10-427-631-2
; Sequence 2, Application US/10427631
; Publication No. US20030175923A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
; APPLICANT: BAUGHN, Mariah R.; LAL, Preeti G.;
; APPLICANT: YUE, Henry; HILLMAN, Jennifer L.;
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592-1 DIV
; CURRENT APPLICATION NUMBER: US/10/427,631
; CURRENT FILING DATE: 2003-04-29
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US99/20989
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: US 60/172,220
; PRIOR FILING DATE: 1999-09-10
; PRIOR FILING DATE: 1998-11-04
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175923A1 2682663CD1
US-10-427-631-2

Query Match 63.5%; Score 1183.5; DB 12; Length 360;
Best Local Similarity 61.2%; Pred. No. 2.4e-216;
Matches 221; Conservative 65; Mismatches 74; Indels 1; Gaps 1;

QY 1 MKALILVGGFGRRLRPLTSLSPKPLVDFANKPMILHQIEALKEGVGVTEVVLAINYRPEVM 60
Db 1 MKALILVGGFGRRLRPLTSLSPKPLVDFANKPMILHQIEALKEGVGVTEVVLAINYRPEVM 60
QY 61 INFLKDFEDKLGITITCSQTEPLEGTAGLALARDKLADGSGQPPFFVLNSDVISSEYPPAE 120
Db 61 EKEMKAQEQRLGIRISMSHSEPELGTAGLALARDLSE-TADPPFVLNSDVICDPFQA 119
QY 121 LIKFKHCHGGEATIMVTKVDSPSKYGVVWMEATGRVERFVEKPKIFVGNKINAGIYLLN 180
Db 120 MYQFRRHGHGQESILVTKVESPSTKYGVVWCEADTGRIRHFRFVEKPOVFSNKNINAGIYLLS 179
QY 181 PSVLDRLELPTSTIEKEVFPQIAADQOLYAMVLPGFMMVGGQPRDYITGLRLYLDLSIRKK 240
Db 180 PAVLARIQLQPTSTIEKEVFPPIVAKESQLYAMELQGFMMVIGQPKDFLGMCLFLQSLRQK 239
QY 241 SAAKLATGAHVGNVNLVHESAKIGEGCLIGPDVAIGPGCVVDEGVRLSRCTVMRGVRIKK 300
Db 240 QPERLCSGPGVGNVNLVDPSPARIGQNCISGPNVSLGPGVWVEDGVCTRRCTVLRDARIRS 299
QY 301 HACISNSIIGHSTVGOWARIEENMTILGEDVHVCDEVYNSGGVVLPHKKEIKSSILKPEIV 360
Db 301 HACISSIIIGHSTVGOWARIEENMTILGEDVHVCDEVYNSGGVVLPHKKEIKSNILKPEIV 360
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Db 300 HSWLESCIWRCRVGQWRMNTVTLGEDVINDELYLNQASVLPKHSIGSVPEPRII 359

QY 361 M 361

Db 360 M 360

RESULT 4

US-10-128-714-8009
; Sequence 8009, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/0128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8009
; LENGTH: 364
; TYPE: PRT
; ORGANISM: *Aspergillus fumigatus*
US-10-128-714-8009

Query Match 62.3%; Score 1161.5; DB 15; Length 364;

Best Local Similarity 60.8%; Pred. No. 5.2e-114;

Matches 222; Conservative 60; Mismatches 78; Indels 5; Gaps 3;

QY 1 MKALILVGGFGTGLRPLTLSPKPLVDFANKPMLHQLHQAIEALKEVGTVTEVVLAINYRPEVM 60

Db 1 MKALILVGGFGTGLRPLTLSPKPLVDFANKPMLHQLHQAIEALKEVGTVTEVVLAINYRPEVM 60

QY 61 INFLKDFEDKLGITITCSQETEPGLTAGPLALARDKLDAGSGQPPFFVLNSDVISSEYPPAE 120

Db 61 VAALKKYEQVNVRIEFSVESEPLGTAGPLKLA-EKILGKDDSPFFVLNSDIIICDYPFKQ 119

QY 121 LIKFKHCHGGEATIMVTKVDEPSKYGVVME-EATGVERFVEKPKIFVGNKINAGIYLL 179

Db 120 LAEPFKHGGDEGTIVVTKVDEPSKYGVVME-EATGVERFVEKPKIFVGNKINAGIYIL 179

QY 180 NPSVLDRLELRPTSTIEKEVFFQIAADQOLYAMVLPFGFMVMDVGPQVITGLRLYLDSIRK 239

Db 180 NPSVLKRIELRPTSTIEQETFAICSDGLHSFDLEGFMVMDVGPQKDFLTGTCLYLASLAK 239

QY 240 KSAAKLATGAHV---GNVLHESNAKIGEGCLIGPDVAIGPCGVVEGVRLSRTVNRGV 296

Db 240 RNSKULAPNSEPYVYGGNVMDPSAKIGKNCRIGNVVGIVGVVGVGLQRCVLENS 299

QY 297 RIKKHACISNSIIGHWSTVGCWARTENMTILGEDVHVCDVYSGVGVVLPKHEIKSSILK 356

Db 300 KYKDHAKWSTIVGNVSSVGNWALENVTLGGDDVTIADENVYNGGSIIPKHSIKQNDIV 359

QY 357 PEIVM 361

Db 360 PAIIM 364

RESULT 5

US-10-032-585-7223
; Sequence 7223, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7223
; LENGTH: 362
; TYPE: PRT
; ORGANISM: *Candida albicans*
US-10-032-585-7223

Query Match 59.0%; Score 1099.5; DB 12; Length 362;

Best Local Similarity 57.9%; Pred. No. 1.9e-107;

Matches 210; Conservative 60; Mismatches 90; Indels 3; Gaps 3;

QY 1 MKALILVGGFGTGLRPLTLSPKPLVDFANKPMLHQLHQAIEALKEVGTVTEVVLAINYRPEVM 60

Db 1 MKGLILVGGYGTRLRPLTLTLPKPLVEFGNRPMLHQLHQAIEALAAAGVTDIVLAINYRPEVM 60

QY 61 INFLKDFEDKLGITITCSQETEPGLTAGPLALARDKLDAGSGQPPFFVLNSDVISSEYPPAE 120

Db 61 VSTLKYYEEYGVISITFSEVEEPJGTASPLKLAEEVLKK-DQSPFFVLNSDVIDCDYPPKE 119

QY 121 LIKFKHCHGGEATIMVTKVDEPSKYGVVME-EAT-GRVERFVEKPKIFVGNKINAGIYLL 179

Db 120 LADPHKARAGAGTIVATKVDEPSKYGVIVHDDTPNLDISRFVEKPVFVGNINAGIYIL 179

QY 180 NPSVLDRLELRPTSTIEKEVFPQAAADQOLYAMVLPFGFMVMDVGPQVITGLRLYLDSIRK 239

Db 180 NPSVIDLIEMRPTSTIEKETPFIIVQKQLYSFDLEGFMVMDVGPQKDFLTGTCLYLISLSK 239

QY 240 KSAAKLATGAHV-VGNVLHESNAKIGEGCLIGPDVAIGPCGVVEGVRLSRTVNRGVRI 298

Db 240 KHPEKCKEYVHGVNLDIDPTAKIHPSALIGENVITGNVVGEGARIQSVLLANSQV 299

QY 299 KKHACISNSIIGHWSTVGCWARTENMTILGEDVHVCDVYSGVGVVLPKHEIKSSILKPE 358

Db 300 KDHAWKSTIVGNVSRIGKWARTEGTVLGGDDVEVKKEIYVNGAKVLPKHSISSNVEKES 359

QY 359 IVM 361

Db 360 IIM 362

RESULT 6

US-10-427-631-33
; Sequence 33, Application US/10427631
; Publication No. US20030175923A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
; APPLICANT: BAUGHN, Mariah R.; LAL, Preeti G.;
; APPLICANT: YUE, Henry; HILLMAN, Jennifer L.;
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PP-0592-1 DIV
; CURRENT APPLICATION NUMBER: US/10/427,631
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: JS 09/786,240
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US99/20989
; PRIOR FILING DATE: 1999-09-03

; PRIOR APPLICATION NUMBER: US 60/172,220
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/155,248
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/133,642
; PRIOR FILING DATE: 1999-05-11
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20030175923A1 g2804432
US-10-427-631-33

Query Match 56.1%; Score 1045; DB 12; Length 373;
Best Local Similarity 55.3%; Pred. No. 1.1e-101;
Matches 203; Conservative 64; Mismatches 92; Indels 8; Gaps 3;
QY 1 MKALILVGGGTRLRPLTLTSPKPLVDFAKPMILHIOEALKEVGVTEVVLAINEYRZEV 60
DB 9 MKALILVGGGTRLRPLTLTQPLVEFAKPMILHIOEALAEVGVDTVVLAISYAEQL 68
QY 61 INFLKDFEDKLGITITCSQETPELGTAGPLALARDKLADGSGQFFVLNSDVISYPPFAE 120
DB 69 EQEMTHADRLGVKLIFSELEPELGTAGPLALARKHL-EGDA-PFFVLNSDVICDFFPKQ 126
QY 121 LKFKHCHGGEATMTKVDPSKYGVVMEETGRVERFVEKPIFVGKNKINAGIYLLN 180
DB 127 MVFEFKHKGEGTIAVTKVEPSKYGVVVDQDKGIDDEVEKPEQEVVGKNKINAGIYIF 186
QY 181 PSVLDRLELPTSTIEKEVFFQIAADQOOLYAMVLPGFMDVQOPRDYITGLRLYLDLSIRKK 240
DB 187 SKILDRIPLEKPTSTIEKEIFPEMAFSGNLAYAFVLPGFMDVQOPKDFLKGMSLFNLHCHTT 246
QY 241 SAAKLTG-----AHVGNVLVHESAKIGEGCLIGDPDVAIGCGVVEDGVRLSRCTVMR 294
DB 247 KSDLETGNSIHPTATIRGNMVDPSATVGNCVIGDPDVGPRVKIEGGVRIHLHSTLS 306
QY 295 GVRKKHACISNIIHGHSTGQWARIENTMILGEDVHVCDVYVNGGVLPKHKEIKSSI 354
DB 307 DSSIGNVSWSGSVGRKCHTGSWRNIECVIGDDVVVMDLYLNGASVLPKHSIAVNV 366
QY 355 LKPEIVM 361
DB 367 PSKDIIM 373

RESULT 7
US-10-128-714-3009
; Sequence 3009, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wendi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899

; PRIOR FILING DATE: 2001-07-39
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3009
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3009

Query Match 47.1%; Score 578.5; DB 15; Length 319;
Best Local Similarity 59.9%; Pred. No. 3.5e-84;
Matches 170; Conservative 45; Mismatches 64; Indels 5; Gaps 3;
QY 75 ITCQETPELGTAGPLALARDKLADGSGQFFVLNSDVISYPPFAELIKFKHCHGGEATI 134
DB 10 IEFVSESEPLGTAGPLKLA-EKILCKDSDSPFFVLNSDIICDYPPKQAEFFKHCHGDEGTI 68
QY 135 MVTKVDEPSKYGVVME-EATGRVERFVEKPIFVGKNKINAGIYLLAPSVLDRLELRPTS 193
DB 69 VTKVDEPSKYGVVVKPNHPSRIDRFVEKPEVFGNRRINAGIYILNPSVLKRIELRPTS 128
QY 194 IEKEVFPQIADQOOLYAMVLPGFMDVQOPRDYITGLRLYLDLSIRKSAALKATGAHV- 252
DB 129 IEQETFPALCSDGQSLDLEGFMDVQOPKDFLTGTCLYLASAKRNSKULAPNSPYV 188
QY 253 --GNVLVHESAKIGEGCLIGDPDVAIGCGVVEDGVRLSRCTVMRGVRIKKHACISNIIIG 310
DB 199 YGVNMVMDPSAKIKNCRCIGPNVWIGPNVVGDVGRVLRQCVLLENSKYKDEAWIKSTIVG 248
QY 311 WHSTVGQWARIENTMILGEDVHVCDVYVNGGVLPKHKEIKSSI 354
DB 249 WNSSVGVKWARLENTVLGDDVTIADDEVYVNGGSLPHKHSIKQNI 292

RESULT 8

US-10-156-761-14505
; Sequence 14505, Application US/1015676;
; Publication No. US20030119018A;
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/-56,762
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14505
; LENGTH: 831
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14505

Query Match 27.6%; Score 515; DB 15; Length 831;
Best Local Similarity 32.4%; Pred. No. 4.3e-45;
Matches 121; Conservative 84; Mismatches 140; Indels 28; Gaps 11;
QY 1 MKALILVGGGTRLRPLTLTSPKPLVDFAKPMILHIOEALKEVGVTEVVLAINEYRZEV 60
DB 1 MKAVVMAGGEGTRLRPMTSSMPKPLPVNRRIMEHVRLRLKRLHGLNETVTVQVFLASLV 60
QY 61 INFLKDFEDKLGITITCSQETPELGTAGPLALARDKLADGSGQFFVLNSDVISYPPFAE 120

Db 61 KNYFGDGEELGMELTAYANE3KPLGTAGSVKNAEBAEKDPT---FLVISCDAITDFDLTE 116
Qy 121 LIKFKHCHGEATIMVTKVDSPSKYGVVWMBEATGRVERFVEKPKIFVGNKINAGIYLLN 180
Db 117 LINFHKEKAGALVTVCLTRVNPFLFEGITIVDE-EGKVERFLEKPTWQVP-SDTVNTGIY 174
Qy 178 LNPVLDRIELRPTSE--KEVFPQIAAD-QOLYAMVLPFGFMDVGPQPDYITG-----229
Db 175 VMEFEVNYVE-ADVSDVMSDVPFQPMKDKPVGIVGAEGYWDVGTSHSYVKAQADVL 233
Qy 230 ---LRLYLDRIKSAAKLATGAHVGNVNLVHESAKIGEGCLIGPDV-----AIGFGCV 280
Db 234 EGKVDVLDGFEISPGVWVAGAEVHPDAVLRGLYIGDYAKVEADVREHTVVGSNV 293
Qy 281 VEDGVLRSCTVMRGVIRIKHACISNIIGHSTVGGWARIENMTILGEDVHVHCVDEYNS 340
Db 294 VKSGAFLHRAVVDVYVIGQHSNLRGCVIGKNTDIMEAARIEDGAVIGDECLVGEESI 353
Qy 341 GGV-VLPHKEIKS 352
Db 354 GNVRYVFKITIEA 366

RESULT 9
US-09-712-363-269
; Sequence 269, Application US/097:2363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712.363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-269
Query Match 26.2%; Score 488; DB 10; Length 359;
Best Local Similarity 34.6%; Pred. No. 8.3e-43;
Matches 125; Conservative 63; Mismatches 151; Indels 22; Gaps 10;
Qy 3 ALILVGGGTGLRLPLTLSPKPLVDFAKPMILHQLKEVGVTEVVLAINRPEVMI 62
Db 8 AWLVGGGTGLRLPLTLSPKPLVDFAKPMILHQLKEVGVTEVVLAINRPEVMI 62
Qy 63 FLKDFED--KLGITTCSETEPLCTAGPLALARDKLDGSGQPFVNLSDVISEYPAE 120
Db 65 FEAEFGDGSALGLQIEYVTEEHLPTGGGIANVAGKLRNDA---MVFNGDVLSDGLAQ 121

Qy 121 LIKFKHCHGEATIMVTKVDSPSKYGVVWMBEATGRVERFVEKPKIFVGNKINAGIYLLN 180
Db 122 LLDHFRSNRADVTQLQVRVGDPRAFGCVPTDE-EDRVVAFLEKTEDEPTDOINAGCVFE 180
Qy 181 PSVLDRI-ELRPTSEIEKEVFPQIAADQ--OLYAMVLPFGFMDVGPQPDYITGLRLYLD 237
Db 181 RNVIDRIFQREVSVEREFPAALLADGDCIKYGVVDASYWRDMGTPEDFVRG---SADLV 237
Qy 238 RKSAAKLATGAHVGNVNLVHESAKIGEGCLIGPDVAGFVGVVDEGVLRSCTVMRGV 297
Db 238 RGIAPSPALRGHR--GEQLVHDGAASPGALLIGGTVWGRCAEIGPGLTGLGAVIFDGV 295
Qy 298 IKHACISNIIGHSTVGGWARIENMTI--LGEDVHVHCVDEYNSG---GVVLPHKEIKS 352
Db 296 VEAGCVIERSIIGFAGRIGPRLIRCGVIGDGADIGARCELLSGARVMPGVFLPDGGIRY 355
Qy 353 \$ 353
Db 356 \$ 356

RESULT 10
US-10-156-761-12571
; Sequence 12571, Application US/10:56761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAEIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156.761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12571
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12571
Query Match 25.2%; Score 469.5; DB 15; Length 360;
Best Local Similarity 32.9%; Pred. No. 7.5e-41;
Matches 114; Conservative 68; Mismatches 147; Indels 17; Gaps 8;
Qy 2 KALILVGGGTGLRLPLTLSPKPLVDFAKPMILHQLKEVGVTEVVLAINRPEVMI 61
Db 3 EAILVGGGTGLRLPLTLVHTKPMVPAAGVPLTHQLARARAAAGVDHIVLATSIAEVE 62
Qy 62 NFLKDFEDKLGITTCSETEPLCTAGPLALARDKLDGSGQPFVNLSDVISEYPAE 121
Db 63 PYFGD-GSALGLHLEYVTEEPLGTGGAINRVARLHSGDPEVLI FNGDILTGDLRAL 121
Qy 122 IKFKHCHGEATIMVTKVDSPSKYGVVWMBEATGRVERFVEKPKI---FVGNKINAGIYL 178
Db 122 VHTHETTAADVSLHLLTKVTDPRAYGLVPTDE-TGRVTAFLKPKPTPEEIVTDQINAGAYV 180
Qy 179 LNPVLDRIEL-RPTSEIEKEVFP-QIAADQOLYAMVLPFGFMDVGPQPDYITGLRLYLD 236
Db 181 FRRSVIDTIPAGRPVSVVERETFPGLLSAGAHLOQGVDSITYWLDLGTFAAFVRG---SADL 237
Qy 237 IRKSAAKLATGAHVGNVNLVHESAKIGEGCLIGPDVAGFVGVVDEGVLRSCTVMRGV 296
Db 238 VLGRAPSPAVPGR--CGDRVLPTASVANSOKLTGGTVGEGAFVGGARIFGSLTILSGA 295

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QY 297 RIKKHACISNSIIGWHTVG-----WARIENMTILGEDVHVDEV 337
Db 296 VWFPGAVITSLGARSVGRSILTAGVIGDGAVIDAGNELRDGV 341

RESULT 11
US-09-738-626-4325
; Sequence 4325, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, WASATO
; APPLICANT: OKAZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738.626
; CURRENT FILING DATE: 2000-12-18
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 00/280988
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 4325
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4325

Query Match 23.1%; Score 431.5; DB 10; Length 348;
Best Local Similarity 31.7%; Pred. No. 7.5e-37;
Matches 113; Conservative 66; Mismatches 158; Indels 19; Gaps 9;

QY 6 LVGGFGRRLRPLTSLFPKPLVDFANKPMILHQLKEVGVTEVTLAINYRPEVM 65
Db 1 MVGGFGRRLRPLTSLFPKPLVDFANKPMILHQLKEVGVTEVTLAINYRPEVM 60

QY 66 DFEDKLGITITCSQETEPGLTAGLALARDKLADGSGQPFVLSVDVISEYPPAEILKPH 125
Db 61 D-GSEWGLEIEYVVEDQPLGTGGGIRNVYDKLRHDTA--IVFNGDVLGADLNSILDTH 116

QY 126 KCHGGEATIMVTKVDEPSKYGVVMEEATGVRFEVKPKIFVGNKINAGIYLLNPSVLD 185
Db 117 REXDADLTMLHLVAVNPRAFSVCVPTDE-DGRVSEFLEKTEDPTDQINAGCYVFKKELIE 175

QY 186 RIEL-REPTSKEKEVFPQIAAD-QQLYAMVLPGFMDVGPDRDVIITGLRLYLDLSIRKKSAA 243
Db 176 QIPAGRAVSVRETFTPOLLEGGKRVGHVDASTWRDMGTSPDSFVRG---SADLVRGIAYS 232

QY 244 KLATGAHVGNVNLVHESAKIEGCLIGPDVAIGPGCVVEDGVRLSCTVMRGVRIKKHAC 303
Db 233 PLLEGK--TGESLVDSAGV3DGVLLGGTVVGRGTGAGCRVDNVTIFDGVTTIEPGAV 230

QY 304 ISNSIIGWHTVGWARIENMTILGEDVHVDEVYNSG-----GVVLPKHEIKSS 353
Db 291 IENSIISGARIGANAHISG-CIIGEAQVARGACELNAGMRVFGVGVIPDSGIRFS 345

RESULT 12
US-09-769-734-33
; Sequence 33, Application US/09769734
; Publication No. US20030143666A1
; GENERAL INFORMATION:
; APPLICANT: Ecopia BioSciences Inc.
```

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; TITLE OF INVENTION: Genetic Locus for Everninomicin Biosynthesis
; FILE REFERENCE: PA 005-US
; CURRENT APPLICATION NUMBER: US/09/769.734
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 355
; TYPE: PRT
; ORGANISM: M. carbonacea
US-09-769-734-33
```

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Query Match 16.8%; Score 314; DB 12; Length 355;
Best Local Similarity 27.2%; Pred. No. 2e-24;
Matches 100; Conservative 68; Mismatches 148; Indels 52; Gaps 12;

QY 1 MKALILVGGFGRRLRPLTSLFPKPLVDFANKPMILHQLKEVGVTEVTLAINYRPEVM 60
Db 1 VKALVLAGGIGSRMRPITHTSKQJIPVANKPVLFPYGJEARIDAGIREVGIIVGSTAPEI 60

QY 61 INFLKDFEDKLGITITCSQETEPGLTAGLALARDKLADGSGQPF----FVLN--SDVIS 114
Db 61 BRAVGD-GSQFGLKVLYLPQDAPRGLGHAVLIARDFLGDDBFVWYLGDNFVLGGINDAVE 119

QY 115 ----EYPPAEILKHKHKGGEATIMVTKVDEPSKYGVVMEEATGVRFEVKPKIFVGN 170
Db 120 RFRERPHQAQL-----MLTKVKDPHAFGIATM-GPDGRVVDVVEEKPRYKSD 165

QY 171 KINAGIYLLNPSVLDRI-ELRPT-----SIEKEVFPQIAADQQLYAMVLPGFMDVGPDR 224
Db 166 LALGVYVYFSPVHAEIAELKPSWRNELEIYDAQWLHDHRRRESTITGFWKDTGSLA 225

QY 225 DYTGLRLYLDLSIRKKSAAKLATGAHVGNVNLVHESAKIEGCLIGPDVAIGPG----- 278
Db 226 DMJEMNRFILSLDSEVSGVSADTEITGRVVIGPGAVITGSRITGP-VVVGAGSIIRNS 284

QY 279 -----CVVEDGVLSRCTVMRGVRIKKHACISNSIIGWHS--TVGOWARIENMT 325
Db 285 QIGPFTSIDCDCTVIDS-EIEQSIVLRGAFIDG-GRIEWSMIGREARLTGPRAPKTYRF 343

QY 326 ILGEDVHV 333
Db 344 VLGDHSEV 351
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```
RESULT 13
US-09-922-683-10
; Sequence 10, Application US/09922683
; Publication No. US20020192793A1
; GENERAL INFORMATION:
; APPLICANT: DECKER, Heinrich
; TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR
; PSEUDO-CLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS
; GLA.O AND THEIR USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,683
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/194,905
```

FILING DATE: 1999-12-01
 APPLICATION NUMBER: DE 19622783.6
 FILING DATE: 07-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Granados, Patricia D.
 REGISTRATION NUMBER: 33 683
 REFERENCE/DOCKET NUMBER: 026083/0193
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 355 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-922-683-10

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Query Match      15.9%; Score 296; DB 10; Length 355;
Best Local Similarity 27.5%; Pred. No. 1.6e-22;
Matches          95; Conservative 58; Mismatches 160; Indels 32; Gaps 9;

Qy      1 MKALILVGGGTRLRPLTLSPFKPLVDFAFNKPMILHQIEALKVEGVTEVLTAIN-YRPEV 59
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      1 VKALVLAGGTGRSLRPFTHTAAKQLLPTANKPVLFPYALESLAAGAAGVREAGVVGAYGRE- 59

Qy     60 MINFLKDFDKLGITTCISQRTPLGTAGLPALARDKLAGSGOPFFVLNSDVISSEYPFA 119
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db     60 -IRELTGDGTAFGLRIITYLHQPRLGLAHAVIARGFLGD---DDFLLYLGDNLPGQVT 115

Qy    120 ELIKFKCHGGEATIMTKVDPSKYGYVMWEEATGRVERFEVKPIFVGNNKINAGIYLL 179
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    116 DFAQSAADPAARALLLTPVADPSAFGAEV-DADGNVLRLEEKPDVPRSSIALIGVYAF 174

Qy    180 NPSVLDRIE-LRPTS-----EKEVFQIADQOLYAMVLPGFMWDVGQCPRDYITGLRLY 233
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    175 SPAVHEAVRAITPSARGELETHAVOMMIDRGLRVRAETTTPRWRDTGSASEDMLEVRHV 234

Qy    234 LDSIRKESAAK-----LATGAHVGNVLVHESAKIGECCGLIGDPVAIG 276
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    235 LDGLEGRIEGKVDAHSITLVGHVRVAEGNIVRGSHVVGPPVLCAGAVTSSNV-VGPY-SIG 293

Qy    277 PGCVVEDGVLRSCTVMRGVHIKKHCACISNISIIHGHSVTGWQARI 321
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db    294 EDCRVEDSA-IEYSVLLRGAAGVCAESRIEASLIQRGA VVGAPRL 337

```

```

RESULT 14
US/10-156-761-8552
/ Sequence 8552, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: IKEDA, HARUO
/ APPLICANT: ISHKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HATTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOT
/ FILE REFERENCE: 249-262
/ CURRENT APPLICATION NUMBER: US/2-0/156
/ CURRENT FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: JP 2001-204
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SEQ ID NO 8552
/ LENGTH: 237
/ TYPE: PRT

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; ORGANISM: Streptomyces avermitilis
; US-10-156-761-8552

Query March 15.1%; Score 281.5; DB 15; Length 237;
Best Local Similarity 30.7%; Pred. No. 3e-21;
Matches 70; Conservative 46; Mismatches 101; Indels 11; Gaps 6

QY 1 MXAILVGGFGRRLRPGLTSLSPKPLVDPANKPMILH-QIEALKEVGVTEVVLAINVRPEV 59
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MXAVILAGGKGVRLRPYTALPKPLVPIGDOHAILETVLPQLAAAGFTGCTTAIGHLGEI 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 60 MYNFLKDPEDKLGITITCSQTEPLGTAGPLALARDKLAGSGQPPFVLNSDVISEYPPA 119
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 IRAYVGD-GSQMGWADVATSESLGTMGPLTMRRLPES----FLVMNGDILTDLDYA 115
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 120 ELIKPHKCHGCEATIMV-KVDEPSKYGVMWEATGRVSEFVEKPKIFVGNKINAGIYLL 179
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 116 DVLRQHRDSGAPLIATYARKVHIDFGVLITQ--AGRVGVCTEKPS--MDYRVSMGVYGL 171
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 180 NPSVLRIEL-RPTSIKEVFPQIADQQLYAMVLPFGFMMDVQCPDY 226
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 172 SRKTLGGVTPGLPLGCFDELVLCLKTNP LPHAYDFDGYWLDIGRPDY 219
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-09-925-637-18
; Sequence 18, Application US/09925637
; Patent No. US2002010338A1
; GENERAL INFORMATION:
; APPLICANT: Choi
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
; FILE REFERENCE: PB560
; CURRENT APPLICATION NUMBER: US/09/925,637
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/151,933
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 08/781,966
; PRIOR FILING DATE: 1997-01-03
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.3
; SEQ ID NO 18
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-637-18

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Query Match	14.9%	Score	277.5	DB 10	Length	453			
Best Local Similarity	27.2%	Pred. No.	2.2e-20						
Matches	106	Conservative	64	Mismatches	146	Indels	73	Gaps	15
QY	3	ALILVGGFGTRLRPETLSFPKPLVDFANKPMILHQIEALKEVGVTEVLAINRPEVMIN	62						
DB	8	AILLAAGKGTMKSKY---KVLHEVAGKPEVHEVLSVKGSGVDQVTVIHGGAE----	60						
QY	63	FLKDPEDKLGITITCSQTEPLGTAGPLAARDKLADGSGQPFPLV-NSDVISEYFAEL	121						
DB	61	----SVKGHGERSLYSFQEEGLGTAHVAQWAKSHLEDEGTTVWCGDPLTKETLVLT	117						
QY	122	IKPHKCHGEATIMTKVDEPSKYGVVMBEATGRVERFVEKEPIFVG----NKNAGIY	177						
DB	118	IAHEDANAQATVLSASIQQPGYGRIV-RNASGRLERIVEEKDATCAEKDINEISSGIF	176						
QY	178	LINPSVLDRIELRPTSIKEVFPQ:ADQQLYAKVLP-----GFMMDVQCPADY----	226						
DB	177	ATNNKTL-----FELCTQKNDNAQGEYLPDV:LSILNDGGIVVEYVRTNDVEE	225						
QY	227	ITGL--RLYLDSIRKSAAKLATCAHVGVNVLVHESAK:GEGCLIGPDVAIGPCGVVEG	284						

Db 226 IMGVNDRVML-SQAEKAMQRTNHHYHMLNGVTIIDP-----DSTVIGPDVTIGSDTVIEPG 280
Qy 285 VRLS-----RCTVVRGVRIKKHACISNSI-----IGWHSTVGOWARIENMTIL 327
Db 281 VRINGRTEIGEDVVIGQYSEINNSTIENGACIQOSVVNDASVGANTKVGFACJRPQAQL 340
Qy 328 GEDVHVCDEVYNSGGVVLPHKEIKSSILK 356
Db 341 GADVKV-----GNFV-----EIKKADLK 358

Search completed: October 9, 2003, 14:08:10
Job time : 32 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:59:16 ; Search time 20 Seconds
(without alignments)
763.711 Million cell updates/sec

Title: US-09-374-967-2
Perfect score: 1864
Sequence: 1 MKALILVGGFGTRLRP-TLS.....GVVLPHEKIKSSILKPEIVM 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapex: 0.5

Searched: 3287.7 seqs, 42310358 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1681	90.2	361	4	US-09-786-240-32
2	1183.5	63.5	360	4	US-09-786-240-2
3	1178	63.2	361	3	US-09-032-372-12
4	1045	56.1	373	4	US-09-786-240-33
5	401	21.5	421	3	US-09-032-372-3
6	307	16.5	355	1	US-08-196-218-34
7	307	16.5	355	1	US-08-681-953-34
8	296	15.9	355	4	US-09-194-905-10
9	261	14.0	233	4	US-09-328-352-7812
10	241.5	13.0	461	4	US-09-134-001C-3316
11	239	12.8	146	4	US-09-370-838-190
12	228.5	12.3	224	4	US-09-199-637A-175
13	227.5	12.2	258	4	US-09-252-991A-17377
14	214	11.5	393	4	US-09-107-532A-6010
15	193	10.4	431	1	US-08-469-202-14
16	193	10.4	431	2	US-08-484-434C-14
17	193	10.4	431	4	US-09-384-361-14
18	191	10.2	431	1	US-08-090-523-4
19	191	10.2	431	1	US-08-398-627-4
20	191	10.2	431	1	US-08-406-858-4
21	191	10.2	431	4	US-08-120-703A-4
22	191	10.2	431	4	US-08-399-023-4
23	191	10.2	431	5	PCT-US91-04036-4
24	191	10.2	431	5	PCT-US94-05275-4
25	191	10.2	488	4	US-09-444-728-2
26	190	10.2	292	3	US-09-320-878-14
27	190	10.2	292	3	US-09-105-537-12

28 190 10.2 292 4 US-09-141-908-16 Sequence 16, Appli
29 190 10.2 292 4 US-09-657-440-14 Sequence 14, Appli
30 190 10.2 3782 3 US-09-105-537-4 Sequence 4, Appli
31 188 10.1 431 1 US-08-090-523-2 Sequence 2, Appli
32 188 10.1 431 1 US-08-398-627-2 Sequence 2, Appli
33 188 10.1 431 1 US-08-406-858-2 Sequence 2, Appli
34 188 10.1 431 4 US-08-120-703A-2 Sequence 2, Appli
35 188 10.1 431 4 US-08-399-023-2 Sequence 2, Appli
36 188 10.1 431 5 PCT-US91-04036-2 Sequence 2, Appli
37 188 10.1 431 5 PCT-US94-05275-2 Sequence 3, Appli
38 186.5 10.0 518 1 US-08-485-241-3 Sequence 3, Appli
39 186.5 10.0 518 2 US-08-874-162-3 Sequence 5, Appli
40 186 10.0 517 2 US-08-485-241-5 Sequence 5, Appli
41 186 10.0 517 2 US-08-874-162-5 Sequence 5, Appli
42 186 10.0 518 1 US-08-299-675-2 Sequence 2, Appli
43 185 9.9 461 4 US-09-328-352-5107 Sequence 5107, Ap
44 183.5 9.8 324 4 US-09-107-532A-4762 Sequence 4762, Ap
45 182.5 9.8 296 4 US-09-107-532A-6365 Sequence 6365, Ap

ALIGNMENTS

RESULT 1
US-09-786-240-32
; Sequence 32, Application: US/39786240
; Patent No. 6558935
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tcm
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUESLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LAU, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: AZIMZAI, Valda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592 PCT
; CURRENT APPLICATION NUMBER: US/09/786,240
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/150,657; Unassigned; 09/186,779; Unassigned; 60/123,647
; PRIOR FILING DATE: 1998-09-10; 1998-09-10; 1998-11-04; 1998-11-04; 1999-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: g2642159
US-09-786-240-32

Query Match 90.2%; Score 1681; DB 4; Length 361;
Best Local Similarity 88.6%; Pred. No. 6.1e-179;
Matches 320; Conservative 22; Mismatches 19; Indels 0; Gaps 0;
QY 1 MKALILVGGFGTRLRP-TLSFPKPLVDVFANKPMTLHQIEALKKEVGVTEVTLAINYREVM 60
DB 1 MKALILVGGFGTRLRP-TLSFPKPLVDVFANKPMTLHQIEALKKEVGVTEVTLAINYREVM 60
QY 61 INFLKDFEDKLGITITCSCTEPLGTAGPLALARDKLDGSGQPFVFLNSDVISEYPPFAE 120
DB 61 LNFJLKDFTKLEIKITCSQETEPGLTAGPLALARDKLDGSGEPFVFLNSDVISEYPLKE 120
QY 121 LKFKHCHGGEGATIMVTKVDEPSKYGVVVMEEATGRVERFVEKPKIFVGKNKINAGIYLLN 180
DB 121 MLEFHKSHGGEGASIMVTKVDEPSKYGVVVMEEATGRVERFVEKPKIYVGKNKINAGIYLLN 180
QY 181 PSVLDRIRLRPTSTEKEVFPQIAAQQLYANVLGFWMDVQCPREYITGLRLYLDLSRKK 240
DB 181 PSVLDRIRLRPTSTEKEVFPQIAAQQLYANVLGFWMDVQCPREYITGLRLYLDLSRKK 240

Dd		180	NPEVDILIEMKPTSIEKETFPIIVEEKOLYISFDLEGFMMDVGQPKDFLSTGVLYLNSLAK	239
Qy		240	KSAAKLATCAHVGVGNVLVHESAKIGEGCLIGPDVAIGPCGVEDGVALSRECTVMRGVRIK	299
Dd		240	RQPKKLATGANIVGNALIDPTAKISSTAKIGPDVVIGPNTVIGDVAITRSVLCNSTIK	299
Qy		300	KIACISNLSIGHMSTVGQWARIENMTILGEDVHVVCDEVYSNGVYLPHKEIKSIILKPFI	359
Dd		300	NHSLVKSTIVGNSTVGQWCRLGYTVLGDDVEVKDEIYINGGRVLPHKISIDNVFKPAL	359
Qy		360	VM	361
Dd		360	IM	361

```

RESULT 4
US-09-786-240-33
; Sequence 33, Application US/09786240
; Patent No. 6558935
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: Lal, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer J.
; APPLICANT: AZIMZAI, Yalda
; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
; FILE REFERENCE: PF-0592 PCT
; CURRENT APPLICATION NUMBER: US/09/786,240
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/150,657; unassigned; 09/186,779; unassigned; 60/233,642
; PRIOR FILING DATE: 1998-09-10; 1998-09-10; 1998-11-04; 1998-11-04; 1999-05-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: G2804432
US-09-786-240-33

```

Query Match.	56.1%;	Score 1045;	DB 4;	Length 373;
Best Local Similarity	55.3%;	Pred. No. 6.3e-102;		
Matches 203;	Conservative 64;	Mismatches 92;	Indels 8;	Gaps 3;

Qy	1	MKALILVGGGCTRLRLPLTLSPKPLVDPAFANKPMILHQIEALKKEVGVTEVVLAINRYEVM	60
Db	9	MKALILVGGYGRURPULTPKPELVFPAFANKPMMLHQMEALAEVGVDTVVLAINSYRAQL	68
Qy	61	INFLQDFEDKLGITITCSQETEPETAGTALALARDKLDAGSGQFFVLNSDVISEYFP	120
Db	69	EQEMTVHADRLGVKLIISLEEEPLGTAGTALARKHL-EGDA-PFVLNSDVICDFPFKQ	126
Qy	121	LIFKHCHGGEATTMTVKDEPSKYGVVWEEATGRVERFVEKPKIFVGKINAGIYILN	180
Db	127	MVEFHKHKGEGTIAVTKVEPSKYGVVVPDQDKGIDDFVEKPEQYGVGNKINAGLIYS	186
Qy	181	PSVLDRLELRPTSEKEVFPQIAADQQLYAMVLPGFWMQVQPDYITGLRLYLDISRKX	240
Db	187	SKILDRPLKPTSEKEIFPEWASGNLYAFVLPGFWMQVQPKDFLKMSLFLNHCHTT	246
Qy	241	SAAKLATG-----AHVVGNYLVHESAKIGEGCLIGPDVAIGPGCVVEDGVRLSRCTVMR	294
Db	247	KSDKLETGSNIHTPATIRGN:WVDPSPATVGCNVCYIGPDVIGPRVKIEGGVRIILHSILS	306
Qy	295	GVRTKGNACTSNSIGWHSTVGQWARIENTMTILGEDVHVCDVTSYNGGVLPHPHKEIKSSI	354
Db	307	DSSIGNYSWVSGSIVGRKCHTGSWVR:ENICVIGDDVVVKDELYNAGASVLPHPKSIAYNV	366

```

QY 355 LKPEIVM 361
   :||
Db 367 PSKDIIIM 373

RESULT 5
US-09-032-372-3
: Sequence 3, Application US/09032372
: Patent No. 6008337
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Yue, Henry
: APPLICANT: Lal, Preel
: TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESS: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/032,372
: FILING DATE: Herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0478 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 421 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: COLANOT73
: CLONE: 1693222
US-09-032-372-3

Query Match 21.5%; Score 401; DB 3;
Best Local Similarity 29.1%; Pred. No. 5.8e-36;
Matches 123; Conservative 61; Mismatches 159;

QY 1 MKALILVGG--FGTRLRPLTLSPKPLVDFANKPMILHQ
   :|||:|||:|||:|||:|||:|||:|||
Db 2 LKAVILGGPKGTRFRPLSFVFKPLFPVAGVPMIQHH
   :|||:|||:|||:|||:|||:|||:|||
QY 58 -EWMINFLKDFEDKLGITITCSQETPLCTAGPLAARD
   :|||:|||:|||:|||:|||:|||:|||
Db 62 DRPLTQFLEAAQQEFNLPRVYLQEFAPLGTGGGLYHFRD
   :|||:|||:|||:|||:|||:|||:|||
QY 117 PRAELIKFKHCHGGEATIMTKVD--EPSKYGVVWMEEA
   :|||:|||:|||:|||:|||:|||:|||
Db 122 PUSAMELRHQRHFFELGLGTTANRTQTSNLYGCIIVENPQ
   :|||:|||:|||:|||:|||:|||:|||
QY 175 GYVILNFSVLI-----DRLELRF-----T

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Db 182 GIYLFSPKALPLRDVFNQDQGLDPSGLWPGAGTIRLEQDVFSALAGQCIYVHLT 241
QY 214 PGFMDVQOPRDYITGLRLYLDSIRKSAKATGAHVGVNVL-----VHESAKIGEGCL 268
Db 242 DGIWSQIKSAGSALYLSRYVQDTHPERLA--KHTPGMPDPRECVPDRQG----- 295
QY 269 IGPDAIAGP-----GCVBDEGYRLSRC--TVNRGVIKHKACISNIIIGHSTVG 316
Db 296 -GPLGCAGPQRLHREGDGRG-RVCGSGRASSMPELCKRSTRV---FCIASWAGGAPWDAG 351
QY 317 QWARIENWTI-----LGEDVHVCDVYVNGGVLPKHKEI 350
Db 352 RAWRVPPVTLPTTPEPAWTVRASSRTGSCCLLSPSMGRCVRIPAEVLIILNSIVLPKHKEI 411
QY 351 KSS 353
Db 412 SRS 414

RESULT 6
US-08-196-218-34
; Sequence 34, Application US/08193218
; Patent No. 5614619
; GENERAL INFORMATION:
; APPLICANT: Piepersberg, Wolfgang
; APPLICANT: Stockmann, Michael
; APPLICANT: Taleghani, Kampiz Mansouri
; APPLICANT: Distler, Jurgen
; APPLICANT: Grabley, Susanne
; APPLICANT: Sichel, Petra
; APPLICANT: Brau, Barbara
; TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
; TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and Their
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196.218
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: 36,228
; REFERENCE/DOCKET NUMBER: 02481.1372-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-196-218-34

Query Match 16.5%; Score 307; DB 1; Length 355;
Best Local Similarity 28.4%; Pred. No. 1.4e-25;
Matches 100; Conservative 59; Mismatches 137; Indels 56; Gaps 12;

QY 1 MKALIVGGGFTRLRPLTSLSPKPLVDPFANKFMIHQIEALKEVGVTEV-VLAINYRPEV 59

Db 1 MKALIVLAGSGTR-LRPSYSMPKQLPIANTVPLVHVNAVRELGVTEVSVIVGNRGPEI 60
QY 60 MINFLKDFEDKLG-----TITCSQETELGTAGPLALARDKLADGSGQPFFVFLNSDVI 113
Db 61 -----EAVLGGCARFDVRITYIPQAPRGLAHTVSIAGFJGD---DDFVWYLGDNK 109
QY 114 SEYPFAELIKFKHCHGGEATINVTIKVDEPSKYGVVVMEEATGRVERFEVFKPIFVGNKIN 173
Db 110 LPDGVTEIAEFTQRPAACVVVHKVPDPRSGVAEL-GPDGEVLRLVEKFWQPRSDMAL 168
QY 174 AGIYLNPVSLDRI-EARPTS-----IEKEVFPQIADQQLYAMVLPGFMDVQOPDIYI 227
Db 169 IGVVFETAAIHQAAVAAISPSRGELEITDAVQWLVTSQADVRLSYDGYWKTGRVEDVL 228
QY 228 TGLRLYLDLSIRKSAKATGAHVGVNVLVHESAK-----ICEGCL-----IGP 271
Db 229 ECNSHLLDGLTFRVDGQVADSVLGVVIEAGARIVRSRVEGPAIIGAGTVLQDSQVGP 288
QY 272 DVAIGPGCVVED-----GVRLSRCTV--MRGVRIKHKACISNIIIGHSTVG 316
Db 289 HTSIGRDCVTDSRLSGSIALDEASVTQVRGLR-----NSLIGRAASVVG 332

RESULT 7
US-08-681-953-34
; Sequence 34, Application US/08681953
; Patent No. 5710032
; GENERAL INFORMATION:
; APPLICANT: Piepersberg, Wolfgang
; APPLICANT: Stockmann, Michael
; APPLICANT: Taleghani, Kampiz Mansouri
; APPLICANT: Distler, Jurgen
; APPLICANT: Grabley, Susanne
; APPLICANT: Sichel, Petra
; APPLICANT: Brau, Barbara
; TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
; TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and Their
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681.953
; FILING DATE: 30-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/196,218
; FILING DATE: 25-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: 36,228
; REFERENCE/DOCKET NUMBER: 02481.1372-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-681-953-34

Query Match 16.5%; Score 307; DB 1; Length 355;
Best Local Similarity 28.4%; Pred. No. 1.4e-25;
Matches 100; Conservative 5%; Mismatches 137; Indels 56; Gaps 12;

QY 1 MKALILVGGFGTRRLRPLTSLSPKPLVDFPANKPMILHJOEALKEVGVTEV-VLA-NYRPEV 59
DB 1 MKALVLAGSGTRRLRPLTSPKPLVDFPANKPMILHJOEALKEVGVTEV-VLA-NYRPEV 60

QY 60 MINFLKDFEDKLG-----ITTCSETEPLGTAGLALARDKLADSGQFFVLNSDVI 113
DB 61 -----EAVLGDGARFDVITYIPQDAPRGLAHTVSIARGLGD---DQFVYLGDNM 109

QY 114 SEYPAELIKFKHCHGGGATIMVKVDEPSKYGVVMEAEATGRVERFVEKPKIFVGNKIN 173
DB 110 LPDGVTEAEETROPAPACVVVHKVPDPFRSGVAEL-GPDGEVLRVLEKPMQPRSDMAL 168

QY 174 AGIYLLNPSVLDRI-ELRPIS-----IEKEVFPQIAADQQLYAMVLPFGFMDVGCPRDYI 227
DB 169 IGVIYFTAAIHQAVAAISPSRGELEITDAVQMLVTSADVRASLYOGYWKOTGRVEDVL 226

QY 228 TGLRVLVLSIRKSAAKLATGAHVGVNVLVHESAK-----IGEGCL-----IGP 271
DB 229 ECNSHLLDGLTPRVDQVADSVLGRVVIIEAGARIVRSRVEGPAIIGAGTVLQDSQWGP 288

QY 272 DVAIGPGCVVED-----GVLRSCTV--MRGVRIKHKHACISNSIIGHSTVG 316
DB 289 HTSIGRDCVTVDLSRLEGSLADEASVTGVRGLR-----NSLIGRAASVG 332

RESULT 8

US-09-194-905-10
; Sequence 10, Application US/09194905
; Patent No. 6306627

GENERAL INFORMATION:

; APPLICANT: DECKER, Heinrich
; TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR
; PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS
; TITLE OF INVENTION: GLA.O AND THEIR USE
; NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/..94.905
; FILING DATE: 29-JUL-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/EP97/02826
; FILING DATE: 30-MAY-1997

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 19622783.6
; FILING DATE: 07-JUN-1996

ATTORNEY/AGENT INFORMATION:

; NAME: Granados, Patricia D
; REGISTRATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 046083/0193

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5399
; TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO:

; INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

; LENGTH: 355 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-194-905-10

Query Match 15.9%; Score 296; DB 4; Length 355;
Best Local Similarity 27.5%; Pred. No. 2.3e-24;
Matches 95; Conservative 58; Mismatches 160; Indels 32; Gaps 9;

QY 1 MKALILVGGFGTRRLRPLTSLSPKPLVDFPANKPMILHJOEALKEVGVTEVWLAIN-YRPEV 59
DB 1 VKALVLAGSGTRRLRPLTSPKPLVDFPANKPMILHJOEALKEVGVTEVWLAIN-YRPEV 59

QY 60 MINFLKDFEDKLGITITTCSETEPLGTAGLALARDKLADSGQFFVLNSDVISEYPPA 119
DB 60 -IRELTGDTAGTFLRITVLHQPRLPLGLAHAVRIARGLGD---DDFLYLGDNVLPQGV 115

QY 120 ELIKFKHCHGGGATIMVKVDEPSKYGVVMEAEATGRVERFVEKPKIFVGNKINAGIYLL 179
DB 116 DFARSAADPAAARLULTPVADPSAPGVAEV-DADGNVLRLEEKDPVPRSSCALIGVTAF 174

QY 180 NPSVLDRIE-LRPTS-----IEKEVFPQIAADQQLYAMVLPFGFMDVGCPRDYITGLRLY 233
DB 175 SPAVHEAVRAITPSARGELEITHAVQMMIDRGLRVRAETTTTPWZDTGSAEDMLEVNRHV 234

QY 234 LSIIRKKSNAK-----LATGAHVGVNVLVHESAKIGEGCLIGPDVAIG 276
DB 235 LDGLEGRIGKVDASHSTLVGRVRAEGAIVRGSHVGVVGVVIGAGAVVSNSS-VGPYTSIG 293

QY 277 PGCVVEDGVRLSRCTVWRGVRIKHKHACISNSIIGHSTVGQWARI 321
DB 294 EDCRVEDSA-IEYVLLRGAQVEGASRIEASJIGRGAVVGPAPRL 337

RESULT 9

US-09-328-352-7812
; Sequence 7812, Application US/09328352
; Patent No. 6562958

GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 7812

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-7812

Query Match 14.0%; Score 261; DB 4; Length 233;
Best Local Similarity 32.7%; Pred. No. 9.4e-21;
Matches 74; Conservative 45; Mismatches 91; Indels 16; Gaps 8;

QY 1 MKALILVGGFGTRRLRPLTSLSPKPLVDFPANKPMILHJOEALKEVGVTEVWLAINYRPEW 60
DB 5 MKAMILAGLGNMRPLTLYTPKPLLEVGGGLVWVHIEKUKIGVTEIVINSAWLADKL 64

QY 61 INFLKDFEDKLGITITTCSETEPLGTAGLALARDKLADSGQFFVLNSDVISEYPPAE 120
DB 65 ISSLGD-GSQFGVDIRWTREEGLETAGGIINALPLLOT---DPFILVNGDVWTTMDF-E 119

QY 121 LKFKHCHGGGATIMVKVDEPSKYGVVMEAEATGRVERFVEKPKIFVGNKIN-AGIYLL 179
DB 120 ALRHKLANDLALHJVL--VDNPKQHPGDFITLLNGRAFAFQDDVK--GENJTFSGSVI 174

QY 180 NPSVLDRIEL--RPTSIEKEVFPQIAADQQLYAMVLPFGFMDVGCQP 223
DB 175 HPKLFQGLEAGKRPPLA---PJKQAMHNQKISGEKLGAWYDVGTGP 217

```
RESULT 10
US-09-134-001C-3316
; Sequence 3316, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3316
; LENGTH: 461
; TYPE: PR1
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3316

Query Match      13.0%; Score 241.5; DB 4; Length 461;
Best Local Similarity 25.7%; Pred. No. 4.2e-18;
Matches 98; Conservative 66; Mismatches 159; Indels 59; Gaps 15;

Qy 3 ALILVGGFGRRLRLTLSPFKPLVDFANKPMILHQIEALKEVGVTEVVLAINRPEYMIN 62
Db 15 AIIAAGKGRMKSKY---KVLHEVAGKPWEHVLNNVKQAGVDQIVTIIGHGAE--- 67
Qy 63 FLKDFEDKLGITITCQETEPGLTAGPLALARDKLAGSGQPFVL-NSDVISPEYPAEL 121
Db 68 ---SVKDTLGNQSLYSFODKSLGTGAHAYKMAHEHLADKEGTLVVCGDTPLTITVQLQSL 124
Qy 122 IKPHKCHGGEATIMVTKVDEPSKYGVVMEATGRVERFVEKPIFVGNK----INAGIV 177
Db 125 IEHSTQSHVTVLSASTINPYGGRIRNH-NGILRIVEEKDANDSEAIKEISSGIP 183
Qy 178 LLNRSVL-DRIELRPTSTIEKEVFOIAADQQLYAMV-PGFMDVGGPRDYIT-----G 229
Db 184 AFNRVLPEKLE-----QVQNDNAQGEYVLPDVLSLILKDGKAEVYCTEDFDEIIG 235
Qy 230 L--RLYLDLSIRKSAK-----LATGAHV--GNVLVHESAKIGEGCLIGPDVAIGPCV 280
Db 236 VNRSLM-SEAKALQORINRVMENGVTIIDPSFTFGTDVKIGIDTTIEFGVRIGGHTT 295
Qy 281 VEDGV-----RLSRCTVMR3VRIRKCHACISNSIIGWHSTVYGOWARIENMTILGEDVHVC 334
Db 296 IEDVWIGQYSINNSTHISNANIKQ-SVINDSIVGENTTVGPFAQLRPGSNLGSSEVKV- 353
Qy 335 DEVYNGGVVLPHEIKKSIUK 356
Db 354 -----GNFV-----EVKKADIK 365

RESULT 11
US-09-370-838-190
; Sequence 190, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/39/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 39/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 146
; TYPE: PR1
; ORGANISM: Homo sapien.
US-09-370-838-190

Query Match      12.8%; Score 239; DB 4; Length 146;
Best Local Similarity 35.9%; Pred. No. 1.3e-18;
Matches 47; Conservative 23; Mismatches 33; Indels 28; Gaps 1;

Qy 251 VVGNVLVHESAKIGEGCLIGPDVAIGPCVVEDGVRLSRCTVMRGVRIRKCHACISNSIIG 310
Db 9  LLGNVYIHTAKVAPSAVLGNPNVSGKVTGVEGVRLRESIVLHGATLQEHCTVLHSIVG 68
Qy 311 WHSTVGOWARIEN-----MTILGEDVHVCDEVYSNGG 342
Db 69  WGSTVGRWARVEGTSDDPNPDPRARYDSESLFKGKLLPAITILGCRVRIPAEVLIILNS 128
Qy 343 VVLPHEIKKSS 353
Db 129 IVLPHEIKLSRS 139

RESULT 12
US-09-199-637A-175
; Sequence 175, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalira
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; FILE REFERENCE: 00786/365002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 224
; TYPE: PR1
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-175

Query Match      12.3%; Score 228.5; DB 4; Length 224;
Best Local Similarity 33.3%; Pred. No. 3.7e-17;
Matches 75; Conservative 39; Mismatches 90; Indels 21; Gaps 8;

Qy 1  MKALLVGGFGRRLRLPLTSLSPKPLVDFANKPMILHQIEALKEVGVTEVVLAINRPEYV 60
Db 1  MKAMILAAAGRGGERMRPTTLHTPKPLIEAAGVPLIERQLLALRQAGVDDVWINHAWLGEQI 60
Qy 61  INFLKDFEDKLGITITCQETEPGLTAGPLALARDKLAGSGQPFV-NSDVISPEYPAE 120
Db 61  EAYLGD-GRSLGR-AYSPEGEPLTGGIFRALPLLGE---QPFLLNGDVWSDFDYSR 116
Qy 121  LIKPHKCHGGEATIMVTKVDEPSKYGVVME-EATGRVERFVEKPIFVGNKINAGIYLL 179
Db 117  L---H-LADGDL-AHLVL--VDKPAHPAGCFHLDAGRGVGTREAG----GNLTVSGIAVL 167
Qy 180  NPSVLDRIELRPTSTIEKEVFOIAADQ---Q-LYAMVLPGFMDVVG 221
Db 168  HPALFEGCQPGAFKAPLRLKRAIAAGRVSGEYH----GQWVDVG 208
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RESULT 13
US-09-252-991A-17377
; Sequence 6010, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17377
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17377

Query Match 12.2%; Score 227.5; DB 4; Length 258;
Best Local Similarity 33.3%; Pred. No. 6.1e-17;
Matches 75; Conservative 39; Mismatches 90; Indels 21; Gaps 8;

QY 1 MKAILVGGFGRTRLPRLTSLSPKPLVDPAFKPMILHQIEALKEVGVTEVVLAINYRPEVM 60
DB 35 MKAMTLAAGRGMRPTTLHPKPLIEAGVPLIERQLLALRQAGVYDWINHAWLGEQI 94
QY 61 INFLDFEDKLGITITCSQETPLTAGPLALARDKLADGSGQPPFVLNSDVISEYPPAE 120
DB 95 EAYLGD-CGRIGGRYAYSPSEPLETGIGIFRALPLGE---QFFLLNGDVNSDFIYSR 150
QY 121 LKFKHKCHGGEATIMVTVDSPSKYGVVYMB-EATGRVEREVEPKIFVGNKNINAGIYLL 179
DB 151 L---HLADGDLHLVL--VDNPAHPAGDFHLDAGRGVGTREAG---GNLTYSGLAVL 201
QY 180 NPSVLDRLELRPTSTEKEVFQIADQ---QLYAMVLPGFMDVVG 221
DB 202 HPALFEGCGPAGFLAPLLRKAIAAGRVSGEYH----GQWVDVG 242

RESULT 14
US-09-107-532A-6010
; Sequence 6010, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
```

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NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6010:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYDROTHERICAL YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (8) LOCATION 1...393
SEQUENCE DESCRIPTION: SEQ ID NO: 6010:
US-09-107-532A-6010

Query Match 11.5%; Score 214; DB 4; Length 393;
Best Local Similarity 25.0%; Pred. No. 3.8e-15;
Matches 92; Conservative 60; Mismatches 150; Indels 66; Gaps 15;

QY 3 ALLILVGGFGRTRLPRLTSLSPKPLVDPAFKPMILHQIEALKEVGVTEVVLAINYRPEVMIN 62
DB 18 AIIILVGGFGRTRLPRLTSLSPKPLVDPAFKPMILHQIEALKEVGVTEVVLAINYRPEVMIN 70
QY 63 FLKDFEDKLGITITCSQETPLTAGPLALARDKLADGSGQPPFVLNSDVISEYPPAE 120
DB 71 ---QVKAQLGERSKVAQAQELGT-GHAYLQAASFLEGGKGTTLVISGDTPLLTETLNN 126
QY 221 LKFKHKCHGGEATIMVTVDSPSKYGVVYMBEATGRVEREVEPKIFVGNKNINAGI 176
DB 127 LFEYHGGKNASATILTAGAENPTGYGRIIRGH-IGIVEKIVEQKDATPEALVQEIINTGT 185
QY 177 YLL-NPSVLDRLELRPTSTEKEVFQIADQ---QLYAMVLPGFMDVVG 222
DB 186 YCFDNEALFDALSKVGTNNAGYEYLTIIILKEEGHTVAAYO-----TDDFEESMG- 238
QY 223 PRDYITGLRLYLDSDIRKXSAALATGAHVGNVNLVHESAKIGEGCLIGPOVAIGPCVVE 282
DB 239 VNDRIALAK--ANEIMRKRIQM---HMVANGVSFVDSAT---TYIDAGVEIGPDTLIE 288
QY 283 DGYRLSRCTVMRG-----VRIKKACIACISNII-----GWHSTVQWARIENMT 325
DB 289 AGVQIQGNTV.GSDCVIGSHSKIVDSRIEDHVVIENSVISSHVKKHADVGPYAHLRPKA 348
QY 326 ILGEDVHV 333
DB 349 EIGENVHI 356

RESULT 15
US-08-469-202-14
; Sequence 14, Application US/08469202
; Patent No. 5750875
; GENERAL INFORMATION:
; APPLICANT: STALKER, DAVID
; TITLE OF INVENTION: GLYCOCEN BIOSYNTHETIC ENZYMES IN PLANTS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CALGENE, INC.
; STREET: 1920 FIFTH STREET
; CITY: DAVIS
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
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/ SOFTWARE: Microsoft Word 5.1 (a)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/469,202
/ FILING DATE: 6-JUNE-95
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/016,881
/ FILING DATE: 11 FEB 1993
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Elizabeth Lassen
/ REGISTRATION NUMBER: 31,845
/ NAME: Donna E. Scherer
/ REGISTRATION NUMBER: 34,719
/ NAME: Carl J. Schwedler
/ REGISTRATION NUMBER: 36,924
/ REFERENCE/DOCKET NUMBER: CGNE 93-2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 916-753-6313
/ TELEFAX: 916-753-1510
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 431 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-469-202-14
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Query Match 10.4%; Score 193; DB 1; Length 431;
Best Local Similarity 22.2%; Pred No. 9.9e-13;
Matches 94; Conservative 61; Mismatches 170; Indels 98; Gaps 15;

QY 3 ALILVGGFGRTRLPRLTLPKPLVDFAFKPMIL-HQIEALKEVGVTGVVLAINYRPEVMI 61
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 22 ALILAGRGTRLKDLTKRAKPAVHFGGKFRIDFALSNCINSGIRRMGVITQYQSHTLV 81
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 NFLK-----DFEDKLGITTCQETEPGLTAGPLALARDKLAGDSGQPPFFVLNS 110
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 82 QHQRGMSFFNEEMNEFVDLPAQORMKGENWYRGTAQVTONLOIRRYKAEYVVLG 141
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 111 DVISEYPPFAELIKFKHCHGGEATI--MVTKVDEPSKYGVVWMBEATGRVERFEKPKIFV 168
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 142 DHIIYQDYSRMLIDHVEKGARCTVACMPVPIEASAFGVMAVDE-NDKIIEFVEKP--- 196
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 169 GNK-----INAGIYLLNPSVL-----DRIELRPTSTIEKEVFPQIAADQQLYA 210
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 197 ANPPSPNDPSKSLASMGIVYFDADLYELLEDDDDSDNSHDFGKOLIPKITEAGLAYA 256
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 211 MVLP-----GFWMGVQPRDYITG-----LRLYLDLSIRKK 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 257 HPFFLSCVQSDPDABFYWRDVGTLWAYKANLDLASVVFELDMYDRNWPRTYNESLPPA 316
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 SAAKLATGAHVGVNVLVHESAKIGEGCLIGPDVAITGPGCVVEDGVRLSRCTWMRGVRIKK 300
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 317 KPVQDRSGSH--GMTL--NSILVSDGCVIS-----GSVVVQSVLFSR-----VRVNS 358
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 HACISNSIIGHWSTVGQWARIENMTI-----LGEDVHVCDVY--SNGGVVLP 347
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 359 FCDIDSAVLLPEVWVGRSCRRCRVIDRACVPIEGMWIGENNAEDARRFYRSEEGIVLVT 418
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 348 KEI 350
Db |||
QY 419 REM 421
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Search completed: October 9, 2003, 14:04:07
Job time : 22 secs